81758

STIC-Biotech/ChemLib

From: Gibbs, Terra
Sent: Wednesday, November 20, 2002 7:46 PM
To: STIC-Biotech/ChemLib
Subject: Seq search

Could you please do a regular sequence search of SEQ ID NO:1 of Serial no. 09/844915?

Terra Gibbs #79523
AU 1635
Mailbox 11E12
306-3221

THANK YOU!

Point of Contact
P Sheppard
Telephone number (703) 308-4499

Searcher:_____
Phone:_____
Location:_____
Date Picked Up:_____
Date Completed: 12/3/02
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.:_____
WWW/Internet:_____
Other (specify):_____

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 07:29:02 ; Search time 2082 Seconds
(without alignments)
194.470 Million cell updates/sec

Title: US-09-844-915-1
Perfect score: 25
Sequence: 1 [illegible] 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No	Score	% Query Match	Length	DB	ID	Description
c	1	20.2	80.8	1068	14	BM920066	BM920066 AGENCOURT
c	2	19.2	76.8	331	14	D47097	D47097 RICS12007A
	3	19.2	76.8	651	10	BB558103	BB558103 BB558103
c	4	18.8	75.2	647	14	BQ033294	BQ033294 UI-1-CF0-
c	5	18.8	75.2	772	9	AA978428	AA978428 LD30550.5
	6	18.6	74.4	113	17	AZ386270	AZ386270 1M0145H07
	7	18.6	74.4	311	10	BB286341	BB286341 BB286341
	8	18.6	74.4	325	13	BI033939	[illegible]
c	9	18.6	74.4	266	14	D46954	D46954 RICS1[illegible]A
c	10	18.6	74.4	440	17	AQ192768	AQ192768 HS[illegible]
	11	18.6	74.4	643	17	AZ361725	AZ361725 1M[illegible]
c	12	18.6	74.4	361	13	BG[illegible]	[illegible]
c	13	18.6	74.4	1076	17	CNS038MZ	AL[illegible]
	14	18.4	73.6	633	17	AG036456	AG036456 [illegible]
	15	18.4	73.6	1101	17	CNS001FM	AL[illegible]
c	16	18.2	72.8	95	9	AI570016	AI570016 [illegible]
c	17	18.2	72.8	147	9	AI802247	AI802247 [illegible]
c	18	18.2	72.8	215	9	AI[illegible]	[illegible]
	19	18.2	72.8	266	9	AA382074	AA382074 EST95[illegible]
c	20	18.2	72.8	288	10	AW[illegible]	[illegible]
c	21	18.2	72.8	337	9	AA917526	AA917526 ol52f[illegible]
c	22	18.2	72.8	367	10	AL[illegible]	[illegible]
c	23	18.2	72.8	368	10	AW468770	[illegible]
c	24	18.2	72.8	384	9	AA993769	[illegible]
c	25	18.2	72.8	390	10	AW[illegible]	[illegible]
c	26	18.2	72.8	392	9	AI206686	[illegible]
	27	18.2	72.8	411	9	AA[illegible]	[illegible]
c	28	18.2	72.8	414	9	AI949161	[illegible]
c	29	18.2	72.8	420	9	AA97[illegible]	[illegible]
c	30	18.2	72.8	431	9	AI[illegible]	[illegible]
c	31	18.2	72.8	444	9	AI363018	[illegible]
c	32	18.2	72.8	446	10	AW[illegible]	[illegible]
c	33	18.2	72.8	447	14	R56634	R56634 [illegible]
c	34	18.2	72.8	449	9	AI870040	[illegible]
c	35	18.2	72.8	454	9	AI634062	[illegible]
c	36	18.2	72.8	454	10	AW003348	[illegible]
c	37	18.2	72.8	468	14	N24746	[illegible]
c	38	18.2	72.8	479	9	AI968162	[illegible]
	39	18.2	72.8	480	9	AA454836	[illegible]
	40	18.2	72.8	482	14	N49015	[illegible]
c	41	18.2	72.8	503	17	FR0016683	[illegible]
	42	18.2	72.8	509	9	AA075795	[illegible]
c	43	18.2	72.8	515	17	FR0014777	[illegible]
c	44	18.2	72.8	517	14	N48287	[illegible]
c	45	18.2	72.8	520	9	AI[illegible]	[illegible]

ALIGNMENTS

```
RESULT 1
BM920066/c
LOCUS       BM920066                1068 bp    mRNA    linear   EST [illegible]
DEFINITION  AGENCOURT_670637 NIH_MGC_[illegible] Homo sapiens cDNA clone IMAGE: [illegible]
            5', mRNA sequence.
ACCESSION   BM920066
VERSION     BM920066.1  GI:19370445
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1068)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12780  row: h  column: 11
            High quality sequence stop: [illegible].
FEATURES             Location/Qualifiers
     source          1..1068
```

```
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5749930"
                     /clone_lib="NIH_MGC_120"
                     /lab_host="DH10B"
                     /note="Organ: pooled pancreas and spleen, Vector:
                     pCMV-SPORT6, Site_1: NotI, Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of spleen and pancreas from 28 yo
                     male.  Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning).  Average insert
                     size 1.5 kb, insert size range 1-2.5 kb.  Library is
                     normalized and enriched for full length clones and was
                     constructed by C. Gruber (Invitrogen) Research Genetics
                     tracking code ???. Note: this is a NIH_MGC Library."
BASE COUNT      277 a    259 c    277 g    212 t      3 others
ORIGIN

  Query Match             ?? ??,  Score ??.?,  DB 14,  Length 1068;
  Best Local Similarity   88.0%;  Pred. No. 2e+02;
  Matches   22;  Conservative    ?;  Mismatches    ?;  Indels    ?;  Gaps    ?;

Qy          1 AGGGACTTTCCGCTGGGGACTTTCC 25
              ||| || |||| |||||| |||||
Db       1056 AGGGATTTTCCACTGGGGATTTTCC 1032


RESULT 2
D47087/c
LOCUS       D47087                   331 bp    mRNA    linear   EST 03-APR-2002
DEFINITION  RICS1220A Rice green shoot Oryza sativa (japonica cultivar-group)
            cDNA, mRNA sequence.
ACCESSION   D47087
VERSION     D47087.1  GI:700790
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 331)
  AUTHORS   Sasaki,T., Miyao,A. and Yamamoto,K.
  TITLE     Rice cDNA from callus 1995
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Takuji Sasaki
            National Institute of Agrobiological Resources
            Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
            305-8602, Japan
            Tel: 81-298-38-7441
            Fax: 81-298-38-7468
            Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
            PROJECT ='RGP'.
FEATURES             Location/Qualifiers
     source          1..331
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone_lib="Rice green shoot"
                     /note="Green shoot (8 days old)"
BASE COUNT       65 a     94 c     88 g     68 t     16 others
ORIGIN

  Query Match             70.8%;  Score 19.2;  DB 14;  Length 331;
  Best Local Similarity   84.0%;  Pred. No. 4.3e+02;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGGACTTTCCGCTGGGGACTTTCC 25
              |||   ||||| |||||||||||||
Db        288 AGGTNTTTTCCACTGGGGACTTTCC 264


RESULT 3
BB558103
LOCUS       BB558103                 651 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB558103 RIKEN full-length enriched, 2 days pregnant adult female
            ovary Mus musculus cDNA clone E330032E13 3', mRNA sequence.
ACCESSION   BB558103
VERSION     BB558103.2  GI:16448868
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 651)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     On Aug 1, 2001 this sequence version replaced gi:9644469.
            Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel. 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res.  10 (10), 1617-1630 (2000)
             Shibata,K., Fujiwake,S., Inoue,K., Tagawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
FEATURES             Location/Qualifiers
     source          1..651
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="E330032E13"
                     /clone_lib="RIKEN full-length enriched, 2 days pregnant
                     adult female ovary"
                     /sex="female"
                     /tissue_type="ovary"
                     /dev_stage="2 days pregnant adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
```

RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTTCTCGAGTTAATTAAATTAATCGCGCGCGCGCGCG 3'] cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I "

BASE COUNT 149 a 137 c 142 g 224 t
ORIGIN

Query Match 76.9%; Score 19.2; DB 10; Length 651;
Best Local Similarity 87.5%; Pred. No. 4.9e-02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGACTTTCCGCTGGGGACTTTCC 25
||||||||| ||||||||||
Db 313 GGGACTTTCTTGTGGGGACTTTCC 336

RESULT 4
BQ033294/c
LOCUS BQ033294 647 bp mRNA linear EST 27-MAR-2002
DEFINITION "UI-1-CF0-axf-h-06-0-UI s1 NCI_CGAP_PlTr1 Mus musculus cDNA clone UI-1-CF0-axf-h-06-0-UI 3', mRNA sequence.
ACCESSION BQ033294
VERSION BQ033294.1 GI:19768573
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 647)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaphs-r@mail.nih.gov
Tissue Procurement: Dr. Minoru Ko, Dr. Janet Rossent, Dr. Jane Rossent
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 1-27, >AT_rich#low_complexity (matched complement) 50-100, >ID3#SINE/ID 116-201, >PRIB1#SINE/Alu
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1..647
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-1-CF0-axf-h-06-0-UI"
/clone_lib="NCI_CGAP_PlTr1"
/tissue_type="TrophoBlast"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker, Site_1: EcoP I, Site_2: Not I; NCI_CGAP_PlTr1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoP I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the dT-18 tail. The sequence tags for this library are GTGTG, ATCAT, GGTTG, GCTTG. For additional information, contact: Bento Soares, bento-soares@uiowa.edu
TAG_LIB=UI-1-CF0
TAG_TISSUE placenta mouse 11.5 12.5 dys
TAG_SEQ=ATCAT"

BASE COUNT 175 a 143 c 173 g 154 t 2 others
ORIGIN

Query Match 76.9%; Score 19.2; DB 14; Length 647;
Best Local Similarity 87.5%; Pred. No. 7.2e-02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTC 25
||||.|| ||| |||||||||||
Db 416 AGGGATTTCCGCTGGGGACTTTC 440

RESULT 5
AA978428/c
LOCUS AA978428 772 bp mRNA linear EST 14-APR-1998
DEFINITION LD30550.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD30550 5prime, mRNA sequence.
ACCESSION AA978428
VERSION AA978428.1 GI:3155844
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 772)
AUTHORS Harvey,T., Brokstein,P., Hong,L., Evans Holm,M., Shu,S., Tsang,S., Lewis,S. and Rubin,G.M.
TITLE BDGP/HHMI Drosophila EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est_info@fruitfly.berkeley.edu.
Plate: 305 row: E column: 2
High quality sequence stop: 633.
FEATURES Location/Qualifiers
source 1..772
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LD30550"
/clone_lib="LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hour mixed stage embryonic"
/lab_host="XL1 Blue"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoR I; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2."

BASE COUNT 288 a 156 c 165 g 162 t 1 others
ORIGIN

Query Match 75.2%; Score 18.8; DB 9; Length 772;
Best Local Similarity 88.0%; Pred. No. 7.4e-02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GACTTTCCGCTGGGGACTTTCC 25
||||||||||.|| ||| ||||
Db 282 GACTTTCCGCTGGGGACTTTCC 261

RESULT 6
AI396270
LOCUS AI396270 113 bp DNA linear HTG 1-JUL-1999
DEFINITION 1M0148H07F Mouse 129S1 pBeloBAC11 library, Mus musculus genomic

```
            clone UUGC1M0145H07 F, DNA sequence
ACCESSION   AZ386270
VERSION     [illegible]
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 113)
  AUTHORS   Dunn,D., A[illegible],A., Parker,M., [illegible],T., Duval,B., Hamil,C.,
            Islam,H., [illegible], Mahmoud,M., [illegible],F., Pedersen,T., Reilly
            ,M., [illegible],M., [illegible],R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            [illegible] Research Bldg., [illegible], SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0145  row: H  column: 07
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 113.
FEATURES             Location/Qualifiers
     source          1..113
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0145H07"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42hv; Purified genomic DNA from M
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|[illegible]|gb|AF[illegible]), a copy number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically competent E. coli XL10 Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 17;  Length 113;
  Best Local Similarity   84.0%;  Pred. No. 6.2e+02;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGGACTTTCCGCTGGGGACTTTCC 25
              |: ||||:|||:||   | |:||||||
Db         35 AGAGACTTTCCCGGAGAGACTTTCC 59


RESULT 7
BB286341
LOCUS       BB286341                311 bp    mRNA    linear   EST [illegible] JUL 2000
DEFINITION  BB286341 RIKEN full length enriched, 2 cells egg Mus musculus cDNA
            clone B020012E15 3', mRNA sequence.
ACCESSION   BB286341
VERSION     BB286341.1  GI:8985790
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 311)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Fujima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,F., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1..311
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="B020012E15"
                     /clone_lib="RIKEN full length enriched, 2 cells egg"
                     /tissue_type="egg"
                     /dev_stage="2 cells"
                     /lab_host="DH10B"
                     /note="Site_1: SalI, Site_2: BamHI, cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3'], cDNA
                     was cleaved with XhoI and BamHI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT       [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN
```

Query Match 74.4%; Score 18.6; DB 10; Length 311;
Best Local Similarity 84.0%; Pred. No. 7.6e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           | ||||||||||||||||||  | ||
Db      35 AAGGACTTTCCGCTGGGGATGTCC 59
```

RESULT 8
BI033939
LOCUS BI033939 325 bp mRNA linear EST 14 JUN 2001
DEFINITION 2V2 NN2004 080301-614 b07 NN2004 Homo sapiens cDNA, mRNA sequence
ACCESSION BI033939
VERSION BI033939.1 GI:14440565
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 325)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Pucher,P., Jorgensel,C.V., O'Hare,M.J., Soares,F., Prentani,P.P., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/getxml?_gi=1&QV1=NN2004_080301-614-b07&t3=2001-03-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 325.
FEATURES Location/Qualifiers
source 1..325
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN2004"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 101 a 54 c 58 g 112 t
ORIGIN

Query Match 74.4%; Score 18.6; DB 13; Length 325;
Best Local Similarity 84.0%; Pred. No. 7.6e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||  |||||| | |||  |||||||
Db       8 AGGTACTTTCCACAGGGTACTTTCC 32
```

RESULT 9
D46954/c
LOCUS D46954 366 bp mRNA linear EST 03-APR-1996
DEFINITION RICS11038A Rice green shoot Oryza sativa (japonica cultivar group) cDNA, mRNA sequence.
ACCESSION D46954
VERSION D46954.1 GI:700663
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar group).
ORGANISM Oryza sativa (japonica cultivar group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 366)
AUTHORS Sasaki,T., Miyao,A. and Yamamoto,K.
TITLE Rice cDNA from callus 1995
JOURNAL Unpublished (1995)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81 298-38-7441
Fax: 81 298 38 7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp
PROJECT: RGP.
FEATURES Location/Qualifiers
source 1..366
/organism="Oryza sativa (japonica cultivar group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
BASE COUNT 76 a 104 c 94 g 73 t 19 others
ORIGIN

Query Match 74.4%; Score 18.6; DB 14; Length 366;
Best Local Similarity 84.0%; Pred. No. 7.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||  |||||| |||||||||||||
Db     286 AGGTCTTTTCCACTGGGGACTTTCC 264
```

RESULT 10
AQ192768/c
LOCUS AQ192768 440 bp DNA linear HSS 24-NOV-1999
DEFINITION HS_2251_B2_H01_MR CIT Approved Human Genomic Sperm Library I Homo sapiens genomic clone Plate 2251 Col 2 Row H, DNA sequence.
ACCESSION AQ192768
VERSION AQ192768.1 GI:4557333
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 440)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616 3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2251 row: H column: 2
Class: BAC ends
High quality sequence stop: 440.

```
FEATURES             Location/Qualifiers
     source          1..440
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate-2251 Col 2 Row-H"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /sex="male"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
BASE COUNT       89 a     97 c    101 g    152 t      1 others
ORIGIN

  Query Match             74.4%;  Score 18.6;  DB 17;  Length 440;
  Best Local Similarity   84.0%;  Pred. No. 8.1e+02;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGGACTTTCCGCTGGGGACTTTCC 25
              ||||||||  ||    |||||||||||
Db        340 AGGGACTTTCCCTAAGGGGACTTTCC 316


RESULT 11
AZ361725
LOCUS       AZ361725                 643 bp    DNA     linear   GSS [illegible]
DEFINITION  [illegible] Mouse 10kb plasmid UUGCIM library Mus musculus genomic
            clone UUGCIM0106J01 R, DNA sequence.
ACCESSION   AZ361725
VERSION     AZ361725.1  GI:10475425
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beeson,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0106  row: J  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 643.
FEATURES             Location/Qualifiers
     source          1..643
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGCIM0106J01"
                     /clone_lib="Mouse 10kb plasmid UUGCIM library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: pWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid F1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT      171 a    149 c    168 g    155 t
ORIGIN

  Query Match             74.4%;  Score 18.6;  DB 17;  Length 643;
  Best Local Similarity   84.0%;  Pred. No. 8.7e+02;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGGACTTTCCGCTGGGGACTTTCC 25
              ||||||||| | | |||||||||
Db        589 AGGGACTTTTCTCAGAGGACTTTCC 613


RESULT 12
BG970339/c
LOCUS       BG970339                 961 bp    mRNA    linear   EST 12-JUN-2001
DEFINITION  602838356F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4973437
            5', mRNA sequence.
ACCESSION   BG970339
VERSION     BG970339.1  GI:14357976
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 961)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10961  row: p  column: 14
            High quality sequence stop: 282.
FEATURES             Location/Qualifiers
     source          1..961
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4973437"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      [illegible] a    17[illegible] c    225 g    [illegible] t
ORIGIN

  Query Match             74.4%;  Score 18.6;  DB 13;  Length 961;
  Best Local Similarity   84.0%;  Pred. No. 9.4e+02;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGGGACTTTCCGCTGGGGACTTTCC 25
              |||| ||  ||||||||| |||||||
Db        898 AGGGGCTCACCGCTGGGAACTTTCC 874


RESULT 13
```

```
CNS038M2/f
LOCUS       CNS038M2                1076 bp    DNA     linear   GSS 15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            005L05 of library 2 from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL232820
VERSION     AL232820.1  GI:7891955
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 1076)
  AUTHORS   Brunet-Crellin,H., Caillon,I., Dasilva,C., Bouneau,L., Fischer,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1076)
  AUTHORS   Brunet-Crellin,H., Caillon,I., Dasilva,C., Fizames,C., Fischer,C.,
            Bouneau,L., Pillault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1076)
  AUTHORS   Genoscope
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1..1076
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="005L05"
                     /clone_lib="G"
                     /note="Genoscope sequence ID   CNPG005CF03XD1-end , T7"
BASE COUNT      [illegible]
ORIGIN

  Query Match             74.4%;  Score 18.6;  DB 17;  Length 1076;
  Best Local Similarity   94.0%;  Pred. No. 2.6e-02;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 AGGGAATTTCCACACGGGACTTTCC 25
           ||||| ||||| |  ||||||||||
Db      42 AGGGAATTTCCACACGGGACTTTCC 18


RESULT 14
AG036456
LOCUS       AG036456                633 bp    DNA     linear   PRI 01-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-012G14.P, genomic survey sequence.
ACCESSION   AG036456
VERSION     AG036456.1  GI:16563220
KEYWORDS    GSS.
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib: PTB Chimpanzee Male
            BAC Library; clone: PTB-012G14.P.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 633)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (03 AUG 2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center, 1st R&D
            1-7-22 Suehiro-cho,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbac@gsc.riken.go.jp, URL:http://bmp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB. This BAC end
            was generated during the R&D process and so, have higher chance of
            in-line tracking errors.
            PRIMERS
                Sequencing: M13Rev
            LIBRARY
                Vector     : pBS145
                R.Site 1   : SacI
                R.Site 2   : SacI
FEATURES             Location/Qualifiers
     source          1..633
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="PTB 012G14.P"
                     /sex="male"
                     /cell_type "lymphoblast"
                     /clone_lib "PTB Chimpanzee Male BAC Library"
BASE COUNT      181 a    167 c    137 g    148 t
ORIGIN

  Query Match             74.4%;  Score 18.6;  DB 17;  Length 633;
  Best Local Similarity   94.0%;  Pred. No. 1.5e-01;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       4 GGGAATTTCCACACGGGACTT 25
           ||||| ||||| |  ||||||
Db     370 GGGAATTTCCACGCTGGGGACT 389


RESULT 15
CNS001FM
LOCUS       CNS001FM                1101 bp    DNA     linear   PAT 17-JUN-2002
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR04F14 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL060844
VERSION     AL060844.1  GI:4939408
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02 JUN 1999) Genoscope - Centre National de Sequencage ;
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information,
            please see: http://www.fruitfly.org/ The BDGP Drosophila
            melanogaster BAC library was prepared by Pieter de Jong's
            laboratory in the Department of Cancer Genetics at the Roswell Park
            Cancer Institute in Buffalo, NY. The library is named RPCI-98 and
            was constructed by partial EcoRI digestion of Drosophila DNA
            provided by the laboratory of Kim Rubin from the isogenic strain y2,
            cn bw sp, the same strain used for the BACR, BACH, P1 and EGT
            libraries. A more detailed description of the library and how to
            order individual BAC clones, the entire library, or filters for
            hybridization from the BACPAC Resource Center can be found at
            http://bacpac.med.buffalo.edu/drosophila.htm.
FEATURES             Location/Qualifiers
```

```
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="BACR04F14"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
BASE COUNT      251 a    171 c    249 g    279 t    148 others
ORIGIN

  Query Match             73.6%;  Score 18.4;  DB 17;  Length 1101;
  Best Local Similarity   73.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 GGGACTTTCCGCTGGGGACTTTCC 25
           : |:|| |:|| |:| | ||||
Db     971 GGSGCTTTCCGCTGGKGCCCTTCC 994


Search completed: December  1, 2002, 08:56:42
Job time : 2094 secs
```

GenCore version 5.1.2

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 07:30:12 ; Search time 55 Seconds
(without alignments)
175.052 Million cell updates/sec

Title: US-09-844-915-1
Perfect score: 25
Sequence: 1 agggactttccgctggggactttcc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	25	100.0	25	10	US-09-844-915-1	Sequence 1, Appli
c	2	25	100.0	25	10	US-09-844-915-2	Sequence 2, Appli
	3	25	100.0	27	10	US-09-766-095-44	Sequence 44, Appl
	4	25	100.0	27	10	US-09-766-095-124	Sequence 124, App
	5	25	100.0	29	9	US-09-992-964-12	Sequence 12, Appl
	6	25	100.0	29	9	US-10-081-280-10	Sequence 10, Appl
	7	25	100.0	29	10	US-09-887-879-12	Sequence 12, Appl
	8	25	100.0	29	10	US-09-993-234-10	Sequence 10, Appl
	9	25	100.0	29	12	US-10-080-455-6	Sequence 6, Appli
	10	25	100.0	29	12	US-10-052-798-4	Sequence 4, Appli
	11	25	100.0	32	10	US-09-031-629A-5	Sequence 5, Appli
	12	25	100.0	2239	9	US-09-747-419-18	Sequence 18, Appl
	13	25	100.0	8933	10	US-09-943-286-3	Sequence 3, Appli
	14	25	100.0	8933	10	US-09-943-286-4	Sequence 4, Appli
	15	25	100.0	8933	10	US-09-943-286-?	Sequence ?, Appli
	16	25	100.0	8937	10	US-09-872-723-8	Sequence 8, Appli
	17	25	100.0	8937	10	US-09-872-723-9	Sequence 9, Appli
	18	25	100.0	9719	10	US-09-737-190A-1	Sequence 1, Appli
	19	23	92.0	23	9	US-09-889-938-3	Sequence 3, Appli
c	20	19.2	76.8	425	10	US-09-779-307-22	Sequence 22, Appl
c	21	19.2	76.8	731	10	US-09-779-307-7	Sequence 7, Appli
	22	18.2	72.8	480	10	US-09-867-701-5137	Sequence 5137, Ap
c	23	18.2	72.8	592	10	US-09-866-562-66	Sequence 66, Appl
	24	17.6	70.4	1954	10	US-09-864-761-4001	Sequence 4001, Ap
	25	17.4	69.6	433	10	US-09-962-416-541	Sequence 541, App
	26	17.4	69.6	433	10	US-09-964-824A-224	Sequence 224, App
	27	17	68.0	[illegible]	10	[illegible]	[illegible]
c	28	17	68.0	5381	10	US-09-751-877-4	Sequence 4, Appli
	29	17	68.0	[illegible]	10	[illegible]-477-3728	Sequence 3728, Ap
c	30	17	68.0	81001	10	US-09-751-877-1	Sequence 1, Appli
	31	16.6	66.4	62944	10	US-09-954-456-2257	Sequence 2257, Ap
	32	16.2	64.8	1632	10	US-09-974-[illegible]-17	Sequence 17, Appl
	33	16.2	64.8	43058	10	US-09-954-456-292	Sequence 292, App
	34	16.2	64.8	43058	10	US-09-954-456-529	Sequence 529, App
	35	16.2	64.8	43059	10	US-09-980-[illegible]	Sequence [illegible], Ap
c	36	16	64.0	130	10	US-09-864-761-20495	Sequence 20495, A
	37	16	64.0	130	10	US-09-864-761-26221	Sequence 26221, A
	38	16	64.0	284	10	US-09-878-174-14612	Sequence 14612, A
c	39	16	64.0	315	9	US-10-079-623-163	Sequence 163, App
c	40	16	64.0	425	10	US-09-779-307-23	Sequence 23, Appl
c	41	16	64.0	471	10	US-09-864-761-3724	Sequence 3724, Ap
	42	16	64.0	492	10	US-09-759-143-199	Sequence 199, App
	43	16	64.0	492	10	US-09-780-669-199	Sequence 199, App
	44	16	64.0	492	10	US-09-930-606-199	Sequence 199, App
	45	16	64.0	492	10	US-09-822-[illegible]-199	Sequence 199, App

ALIGNMENTS

RESULT 1
US-09-844-915-1
; Sequence 1, Application US/09844915
; Patent No. US20020048564A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Lu, Lina
; APPLICANT: Giannoukakis, Nick
; TITLE OF INVENTION: THE USE OF TOLEROGENIC DENDRITIC CELLS
; TITLE OF INVENTION: FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
; TITLE OF INVENTION: MAKING THE SAME
; FILE REFERENCE: AF31737 / 072396.0225
; CURRENT APPLICATION NUMBER: US/09/844,915
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: [illegible],479
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-1

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGGGACTTTCCGCTGGGGACTTTCC 25
              |||||||||||||||||||||||||
Db          1 AGGGACTTTCCGCTGGGGACTTTCC 25
```

RESULT 2
US-09-844-915-2/c
; Sequence 2, Application US/09844915
; Patent No. US20020048564A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Lu, Lina

```
;  APPLICANT:  Giannoukakis, Nick
;  TITLE OF INVENTION: THE USE OF TOLEROGENIC DENDRITIC CELLS
;  TITLE OF INVENTION:  FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
;  TITLE OF INVENTION:  MAKING THE SAME
;  FILE REFERENCE: AP32737 / 0.2196.0225
;  CURRENT APPLICATION NUMBER:  US/09/844,915
;  CURRENT FILING DATE:  2001-04-27
;  PRIOR APPLICATION NUMBER: 60/200,473
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;    LENGTH: 25
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Cytokine Inducing Immunostimulatory
US-09-844-915-2

  Query Match             100.0%;  Score 25;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.0053;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db      25 AGGGACTTTCCGCTGGGGACTTTCC 1


RESULT 3
US-09-766-095-44
; Sequence 44, Application US/09766095
; Patent No. US20020016A1
;   GENERAL INFORMATION:
;        APPLICANT: Sherrol H. McDonough, Thomas P. Ryder,
;                   Yeasing Yang
;        TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
;                            OLIGONUCLEOTIDES AND PROBES
;                            TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
;        NUMBER OF SEQUENCES: 139
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 611 West Sixth Street
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: USA
;             ZIP: 90017
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
;             COMPUTER: IBM PS/2 Model 50Z or 55SX
;             OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
;             SOFTWARE: WordPerfect (Version 5.0)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/766,095
;             FILING DATE: 18-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/013,406
;             FILING DATE: 26-JAN-01
;             APPLICATION NUMBER: U.S. Serial No. US20020016A1 07/550,837
;             FILING DATE: 10-Jul-90
;             APPLICATION NUMBER: U.S. Serial No. US20020016A1 07/373,501
;             FILING DATE: 11 Jul 89
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 196/189
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 44:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 27
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-766-095-44

  Query Match             100.0%;  Score 25;  DB 10;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0053;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       3 AGGGACTTTCCGCTGGGGACTTTCC 27


RESULT 4
US-09-766-095-124
; Sequence 124, Application US/09766095
; Patent No. US20020016A1
;   GENERAL INFORMATION:
;        APPLICANT: Sherrol H. McDonough, Thomas P. Ryder,
;                   Yeasing Yang
;        TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
;                            OLIGONUCLEOTIDES AND PROBES
;                            TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
;        NUMBER OF SEQUENCES: 139
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 611 West Sixth Street
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: USA
;             ZIP: 90017
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
;             COMPUTER: IBM PS/2 Model 50Z or 55SX
;             OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
;             SOFTWARE: WordPerfect (Version 5.0)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/766,095
;             FILING DATE: 18-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/013,406
;             FILING DATE: 26-JAN-01
;             APPLICATION NUMBER: U.S. Serial No. US20020016A1 07/550,837
;             FILING DATE: 10-Jul-90
;             APPLICATION NUMBER: U.S. Serial No. US20020016A1 07/373,501
;             FILING DATE: 11 Jul 89
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 196/189
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 124:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 27
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 124:
US-09-766-095-124

  Query Match             100.0%;  Score 25;  DB 10;  Length 27;
  Post Local Similarity   72.0%;  Pred. No. 0.0053;
  Matches   18;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           ||||||...||||.||||||...|| 
Db       3 AGGGACUUUCCGCUGGGGACUUUCC 27
```

RESULT 5
US-09-992-964-12
; Sequence 12, Application US/09992964
; Patent No. US20020165157A1
; GENERAL INFORMATION
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2DcR
; FILE REFERENCE: P1110
; CURRENT APPLICATION NUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 09/879,169
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 12
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-992-964-12

Query Match 100.0%; Score 25; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 4 AGGGACTTTCCGCTGGGGACTTTCC 28

RESULT 6
US-10-081-280-10
; Sequence 10, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LT AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,077
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/355-8881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-081-280-10

Query Match 100.0%; Score 25; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 4 AGGGACTTTCCGCTGGGGACTTTCC 28

RESULT 7
US-09-887-879-12
; Sequence 12, Application US/09887879
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo 2DcR
; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/879,169
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 12
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-887-879-12

Query Match 100.0%; Score 25; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 4 AGGGACTTTCCGCTGGGGACTTTCC 28

RESULT 8
US-09-993-234-10
; Sequence 10, Application US/09993234
; Patent No. US20021465[illegible]68A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo 2 LT AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: [illegible] No. US20021465[illegible]68A1 2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

```
;               APPLICATION NUMBER: US/09/844,915
;               FILING DATE: <Unknown>
;          ATTORNEY/AGENT INFORMATION:
;               NAME: Marschang, Diane L.
;               REGISTRATION NUMBER: 35,600
;               REFERENCE/DOCKET NUMBER: P1101R1
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: 415/225-5416
;               TELEFAX: 415/882-8881
;               TELEX: 910/371-7168
;     INFORMATION FOR SEQ ID NO: 10:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 29 base pairs
;               TYPE: Nucleic Acid
;               STRANDEDNESS: Single
;               TOPOLOGY: Linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-993-234-10

  Query Match             100.0%;  Score 25;  DB 10;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 9
US-10-080-455-6
; Sequence 6, Application US/10080455
; Patent No. US20020146389A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Baker, Kevin P.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Mark, Melanie R.
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  TITLE OF INVENTION:  DNA[illegible] Polypeptides, A Tumor Necrosis Factor Homolog
;  FILE REFERENCE: P1158R2
;  CURRENT APPLICATION NUMBER: US/10/080,455
;  CURRENT FILING DATE:  2002-02-22
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1998-11-18
;  PRIOR APPLICATION NUMBER: US 60/069,661
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: US 60/065,035
;  PRIOR FILING DATE: 1997-11-18
;  NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 6
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1-29
;   OTHER INFORMATION: Description of Unknown Organism. Unknown
US-10-080-455-6

  Query Match             100.0%;  Score 25;  DB 10;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 10
US-10-052-798-4
; Sequence 4, Application US/10052798
; Patent No. US20020150985A1
;  GENERAL INFORMATION:
;       APPLICANT: Adams, Camilla W.
;                  Ashkenazi, Avi J.
;                  Chuntharapai, Anan
;                  Kim, Kyung J.
;       TITLE OF INVENTION: Apo 2 Receptor
;       NUMBER OF SEQUENCES: 14
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/052,798
;            FILING DATE: 02-Nov-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/079,029
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Marschang, Diane L.
;            REGISTRATION NUMBER: 35,600
;            REFERENCE/DOCKET NUMBER: P1101R2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5416
;            TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 29 base pairs
;            TYPE: Nucleic Acid
;            STRANDEDNESS: Single
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-052-798-4

  Query Match             100.0%;  Score 25;  DB 12;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.0054;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 11
US-09-031-629A-5
; Sequence 5, Application US/09031629A
; Patent No. US20020106689A1
; GENERAL INFORMATION:
;  APPLICANT:  Faustman
;  APPLICANT:  Hayashi
;  TITLE OF INVENTION:  Methods for Treating and Diagnosing Autoimmune Disease
;  FILE REFERENCE:  MGH/Faustman 17633/1030
;  CURRENT APPLICATION NUMBER: US/09/031,629A
;  CURRENT FILING DATE:  1998-02-21
;  NUMBER OF SEQ ID NOS:  6
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 32
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Probe for
;   OTHER INFORMATION: wild type kappa B1 sequence
US-09-031-629A-5
```

Query Match 100.0%; Score 25; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 6 AGGGACTTTCCGCTGGGGACTTTCC 30

RESULT 12
US-09-747-419-18
; Sequence 18, Application US/09747419
; Patent No. US20020155582A1
; GENERAL INFORMATION:
; APPLICANT: Lemon, Stanley
; APPLICANT: Yi, MinKyung
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265.0007.0101
; CURRENT APPLICATION NUMBER: US/09/747,419
; CURRENT FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/171,309
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 2239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of HIVSEAP
US-09-747-419-18

Query Match 100.0%; Score 25; DB 9; Length 2239;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 532 AGGGACTTTCCGCTGGGGACTTTCC 556

RESULT 13
US-09-943-286-3
; Sequence 3, Application US/09943286
; Patent No. US20020106668A1
; GENERAL INFORMATION:
; APPLICANT: Nunomura, Kiyotada
; TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
; FILE REFERENCE: GP104-02.UT
; CURRENT APPLICATION NUMBER: US/09/943,286
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8933
; TYPE: RNA
; ORGANISM: Human Immunodeficiency Virus
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)...(8933)
; OTHER INFORMATION: Sequence of transcripts produced from the BH10
; OTHER INFORMATION: plasmid.
US-09-943-286-3

Query Match 100.0%; Score 25; DB 10; Length 8933;
Best Local Similarity 72.0%; Pred. No. 0.012;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
|||||:::|||:|||||:::|
Db 8790 AGGGACUUUCCGCUGGGGACUUUCC 8814

RESULT 14
US-09-943-286-4
; Sequence 4, Application US/09943286
; Patent No. US20020106668A1
; GENERAL INFORMATION:
; APPLICANT: Nunomura, Kiyotada
; TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
; FILE REFERENCE: GP104-02.UT
; CURRENT APPLICATION NUMBER: US/09/943,286
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 8933
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the IAC-Asis pseudo target
; NAME/KEY: mutation
; LOCATION: (4134)...(4135)
; OTHER INFORMATION: Mutated positions: 4134, 4135, 4136, 4137,
; OTHER INFORMATION: 4152-3, 4155
US-09-943-286-4

Query Match 100.0%; Score 25; DB 10; Length 8933;
Best Local Similarity 72.0%; Pred. No. 0.012;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
|||||:::|||:|||||:::|
Db 8790 AGGGACUUUCCGCUGGGGACUUUCC 8814

RESULT 15
US-09-943-286-9
; Sequence 9, Application US/09943286
; Patent No. US20020106668A1
; GENERAL INFORMATION:
; APPLICANT: Nunomura, Kiyotada
; TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
; FILE REFERENCE: GP104-02.UT
; CURRENT APPLICATION NUMBER: US/09/943,286
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 8933
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the IAI Pol1 pseudo target
; NAME/KEY: mutation
; LOCATION: (4140)...(4159)
; OTHER INFORMATION: Mutated positions: 4147, 42, 4148, 47, 4152,
; OTHER INFORMATION: 4156-57, 4159
US-09-943-286-9

Query Match 100.0%; Score 25; DB 10; Length 8933;
Best Local Similarity 72.0%; Pred. No. 0.012;
Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
|||||:::|||:|||||:::|
Db 8790 AGGGACUUUCCGCUGGGGACUUUCC 8814

Search completed: December 1, 2002, 08:07:47
Job time : 56 secs

SenCore version 5.1.2

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 06:29:17 ; Search time 51 Seconds
(without alignments)
150.332 Million cell updates/sec

Title: US-09-844-915-1
Perfect score: 25
Sequence: 1 agggacttccagaaagggacttccc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	100.0	27	1	US-08-479-852-44	Sequence 44, Appl
2	25	100.0	27	1	US-08-479-852-124	Sequence 124, App
3	25	100.0	27	2	US 08 462 646 44	Sequence 44, Appl
4	25	100.0	27	2	US-08-462-646-124	Sequence 124, App
5	25	100.0	27	2	US-08-484-478-7	Sequence 7, Appli
6	25	100.0	27	2	US-08-353-476-8	Sequence 8, Appli
7	25	100.0	27	4	US-09-013-406-44	Sequence 44, Appl
8	25	100.0	27	4	US-09-013-406-124	Sequence 124, App
9	25	100.0	29	4	US-09-070-020-4	Sequence 4, Appli
10	25	100.0	29	4	US-08-828-060-14	Sequence 14, Appl
11	25	100.0	29	4	US-08-828-683A-10	Sequence 10, Appl
12	25	100.0	33	1	US-08-484-147A-26	Sequence 26, Appl
13	25	100.0	33	2	US-08-484-147A-26	Sequence 26, Appl
14	25	100.0	36	1	US-08-465-590-142	Sequence 142, App
15	25	100.0	36	4	US-08-711-417A-142	Sequence 142, App
16	25	100.0	36	5	PCT/US93/08743 142	Sequence 142, App
17	25	100.0	37	2	US-08-353-476-38	Sequence 38, Appl
18	25	100.0	44	1	US-08-353-476-24	Sequence 24, Appl
19	25	100.0	44	2	US 08-353-476-25	Sequence 25, Appl
20	25	100.0	44	4	US-09-314-691-9	Sequence 9, Appli
21	25	100.0	45	2	US-08-580-998A-12	Sequence 12, Appl
22	25	100.0	45	2	US-08-353-476-19	Sequence 19, Appl
23	25	100.0	45	2	US-08-353-476-23	Sequence 23, Appl
24	25	100.0	45	2	US-08-353-476-26	Sequence 26, Appl
25	25	100.0	46	1	US-08-353-476-20	Sequence 20, Appl
26	25	100.0	46	2	US-08-353-476-21	Sequence 21, Appl
27	25	100.0	46	2	US 08 353 476 22	Sequence 22, Appl
28	25	100.0	46	2	US-08-353-476-27	Sequence 27, Appl
29	25	100.0	60	2	US-08-353-476-45	Sequence 45, Appl
30	25	100.0	70	2	US-08-353-476-34	Sequence 34, Appl
31	25	100.0	70	2	US-08-353-476-37	Sequence 37, Appl
32	25	100.0	72	2	US-08-674-588-4	Sequence 4, Appli
33	25	100.0	74	3	US-08-388-313-647	Sequence 647, Appl
34	25	100.0	82	3	US-08-488-551B-647	Sequence 647, Appl
35	25	100.0	100	2	US-08-353-476-47	Sequence 47, Appl
36	25	100.0	242	1	US-08-171-386-627	Sequence 627, Appl
37	25	100.0	242	1	US-07-966-093-27	Sequence 27, Appl
38	25	100.0	242	1	US-08-484-499-27	Sequence 27, Appl
39	25	100.0	242	1	US-08-123-936-627	Sequence 627, Appl
40	25	100.0	242	1	US-08-476-211B-27	Sequence 27, Appl
41	25	100.0	242	1	US-08-476-876-27	Sequence 27, Appl
42	25	100.0	242	2	US-08-476-228A-627	Sequence 627, Appl
43	25	100.0	242	3	US-08-182-088A-627	Sequence 627, Appl
44	25	100.0	242	4	US-09-454-943-627	Sequence 627, Appl
45	25	100.0	242	5	PCT/US93/12388 627	Sequence 627, Appl

ALIGNMENTS

RESULT 1
US-08-479-852-44
; Sequence 44, Application US/08479852
; Patent No. 5712385
; GENERAL INFORMATION:
; APPLICANT: Sherrol H. McDonough, Thomas E. Ryder,
; APPLICANT: Yeasing Yang
; TITLE OF INVENTION: MULTIPLE AMP APPLICATION
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
; TITLE OF INVENTION: TO BOOST IMMUNOGENICITY OF HIV-1 TYPE 1
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 70-A 21 MHz
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0
; SOFTWARE: WordPerfect (Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,852
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,745
; FILING DATE:
; APPLICATION NUMBER: U.S. Serial No. 5712385 07/465,[illegible]
; FILING DATE: 2/11/90
; APPLICATION NUMBER: U.S. Serial No. 5712385 07/379,571
; FILING DATE: 7/11/89
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 196/183
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-479-852-44

```
  Query Match             100.0%;  Score 25;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       3 AGGGACTTTCCGCTGGGGACTTTCC 27


RESULT 2
US 08 479 852-124
; Sequence 124, Application US/08479852
; Patent No. 5712385
; GENERAL INFORMATION.
;   APPLICANT:  Sherrol H. McDonough, Thomas B. Ryder,
;   APPLICANT:  Yeasing Yang
;   TITLE OF INVENTION:  NUCLEIC ACID AMPLIFICATION
;   TITLE OF INVENTION:  OLIGONUCLEOTIDES AND PROBES
;   TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
;   NUMBER OF SEQUENCES:  139
;   CORRESPONDENCE ADDRESS.
;     ADDRESSEE:  Lyon & Lyon
;     STREET:  611 West Sixth Street
;     CITY:  Los Angeles
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  90017
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;     COMPUTER:  IBM PS/2 Model 50Z or 55SX
;     OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;     SOFTWARE:  WordPerfect (Version 5.0)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/479,852
;     FILING DATE:
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA.
;     APPLICATION NUMBER:  US/08/340,745
;     FILING DATE:
;     APPLICATION NUMBER:  U.S. Serial No. 5712385 07/553,837
;     FILING DATE:  7/10/90
;     APPLICATION NUMBER:  U.S. Serial No. 5712385 07/379,501
;     FILING DATE:  7/11/89
;   ATTORNEY/AGENT INFORMATION.
;     NAME:  Warburg, Richard J.
;     REGISTRATION NUMBER:  32,327
;     REFERENCE/DOCKET NUMBER:  196/189
;   TELECOMMUNICATION INFORMATION
;     TELEPHONE:  (213) 489-1600
;     TELEFAX:  (213) 955-0440
;     TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  124.
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  27
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
US 08 479 852 124

  Query Match             100.0%;  Score 25;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       3 AGGGACTTTCCGCTGGGGACTTTCC 27


RESULT 3
US 08 462 646 44
; Sequence 44, Application US/08462646
; Patent No. 5856088
; GENERAL INFORMATION.
;   APPLICANT:  Sherrol H. McDonough, Thomas B. Ryder,
;   APPLICANT:  Yeasing Yang
;   TITLE OF INVENTION:  NUCLEIC ACID AMPLIFICATION
;   TITLE OF INVENTION:  OLIGONUCLEOTIDES AND PROBES
;   TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
;   NUMBER OF SEQUENCES:  139
;   CORRESPONDENCE ADDRESS.
;     ADDRESSEE:  Lyon & Lyon
;     STREET:  611 West Sixth Street
;     CITY:  Los Angeles
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  90017
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;     COMPUTER:  IBM PS/2 Model 50Z or 55SX
;     OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;     SOFTWARE:  WordPerfect (Version 5.0)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/462,646
;     FILING DATE:  05-JUN-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/040,745
;     FILING DATE:  26-MAR-1993
;     APPLICATION NUMBER:  U.S. Serial No. 5856088 07/550,837
;     FILING DATE:  7/10/90
;     APPLICATION NUMBER:  U.S. Serial No. 5856088 07/379,501
;     FILING DATE:  7/11/89
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Warburg, Richard J.
;     REGISTRATION NUMBER:  32,327
;     REFERENCE/DOCKET NUMBER:  196/189
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (213) 489-1600
;     TELEFAX:  (213) 955-0440
;     TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  44.
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  27
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
US 08 462 646 44

  Query Match             100.0%;  Score 25;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       3 AGGGACTTTCCGCTGGGGACTTTCC 27


RESULT 4
US 08 462 646 124
; Sequence 124, Application US/08462646
; Patent No. 5856088
; GENERAL INFORMATION:
;   APPLICANT:  Sherrol H. McDonough, Thomas B. Ryder,
;   APPLICANT:  Yeasing Yang
;   TITLE OF INVENTION:  NUCLEIC ACID AMPLIFICATION
;   TITLE OF INVENTION:  OLIGONUCLEOTIDES AND PROBES
;   TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
;   NUMBER OF SEQUENCES:  139
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Lyon & Lyon
;     STREET:  611 West Sixth Street
;     CITY:  Los Angeles
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  90017
;   COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;       COMPUTER:  IBM PC/2 Model 50Z or 55SX
;       OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;       SOFTWARE:  WordPerfect (Version 5.0)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/462,646
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/040,745
;       FILING DATE:  26-MAR-1993
;       APPLICATION NUMBER:  U.S. Serial No.  585,098; 07/193,847
;       FILING DATE:  7/10/90
;       APPLICATION NUMBER:  U.S. Serial No:  585,098; 07/376,501
;       FILING DATE:  7/11/89
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard J.
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  196/189
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  124:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  27
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-462-646 124

  Query Match             100.0%;  Score 25;  DB 3;  Length 27;
  Best Local Similarity   92.6%;  Pred. No. 0.0012;
  Matches   18;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           ||||:::|||:|||||:::|
Db       3 AGGGACUUUCCGCUGGGGACUUUCC 27


RESULT 5
US-08-353-476-7
; Sequence 7, Application US/08353476
; Patent No. 5871902
;  GENERAL INFORMATION:
;    APPLICANT:  Weininger, Susan
;    APPLICANT:  Weininger, Arthur M
;    TITLE OF INVENTION:  METHOD OF DETECTION OF DNA WITH A
;    TITLE OF INVENTION:  SPECIFIC SEQUENCE PROBE
;    NUMBER OF SEQUENCES:  117
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik & Saliwanchik
;      STREET:  2421 N.W. 41st St., Suite A-1
;      CITY:  Gainesville
;      STATE:  Florida
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/353,476
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bencen, Gerard H
;      REGISTRATION NUMBER:  34,746
;      REFERENCE/DOCKET NUMBER:  GP-100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (904) 375-8100
;      TELEFAX:  (904) 372-5800
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-353-476-7

  Query Match             100.0%;  Score 25;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       2 AGGGACTTTCCGCTGGGGACTTTCC 26


RESULT 6
US-08-353-476-8
; Sequence 8, Application US/08353476
; Patent No. 5871902
;  GENERAL INFORMATION:
;    APPLICANT:  Weininger, Susan
;    APPLICANT:  Weininger, Arthur M
;    TITLE OF INVENTION:  METHOD OF DETECTION OF DNA WITH A
;    TITLE OF INVENTION:  SPECIFIC SEQUENCE PROBE
;    NUMBER OF SEQUENCES:  117
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik & Saliwanchik
;      STREET:  2421 N.W. 41st St., Suite A-1
;      CITY:  Gainesville
;      STATE:  Florida
;      COUNTRY:  USA
;      ZIP:  32606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/353,476
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bencen, Gerard H
;      REGISTRATION NUMBER:  34,746
;      REFERENCE/DOCKET NUMBER:  GP-100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (904) 375-8100
;      TELEFAX:  (904) 372-5800
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-353-476-8

  Query Match             100.0%;  Score 25;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       2 AGGGACTTTCCGCTGGGGACTTTCC 26
```

```
RESULT 7
US-09-013-406-44
; Sequence 44, Application US/09013406
; Patent No. 6252059
;  GENERAL INFORMATION:
;    APPLICANT:  Cherrol H. McDonough, Thomas B. Ryder,
,    APPLICANT:  Yeasing Yang
,    TITLE OF INVENTION:  NUCLEIC ACID AMPLIFICATION
,    TITLE OF INVENTION:  OLIGONUCLEOTIDES AND PROBES
,    TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
;    NUMBER OF SEQUENCES:  139
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/013,406
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/479,852
;      FILING DATE:
;      APPLICATION NUMBER:  U.S. Serial No.: 6252059 07/550,837
;      FILING DATE:  7/10/90
;      APPLICATION NUMBER:  U.S. Serial No.: 6252059 07/479,501
;      FILING DATE:  7/11/89
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  196/189
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-013-406-44

  Query Match             100.0%;  Score 25;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       3 AGGGACTTTCCGCTGGGGACTTTCC 27


RESULT 8
US-09-013-406-124
; Sequence 124, Application US/09013406
; Patent No. 6252059
;  GENERAL INFORMATION:
;    APPLICANT:  Cherrol H. McDonough, Thomas B. Ryder,
;    APPLICANT:  Yeasing Yang
;    TITLE OF INVENTION:  NUCLEIC ACID AMPLIFICATION
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES AND PROBES
;    TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
;    NUMBER OF SEQUENCES:  139
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/013,406
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/479,852
;      FILING DATE:
;      APPLICATION NUMBER:  U.S. Serial No.: 6252059 07/550,837
;      FILING DATE:  7/10/90
;      APPLICATION NUMBER:  U.S. Serial No.: 6252059 07/479,501
;      FILING DATE:  7/11/89
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  196/189
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  124:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-013-406-124

  Query Match             100.0%;  Score 25;  DB 4;  Length 27;
  Best Local Similarity   92.6%;  Pred. No. 0.0012;
  Matches   18;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           ||||||:::|||||:|||||:::|| |
Db       3 AGGGACUUUCCGCUGGGGACUUUCC 27


RESULT 9
US-09-079-029-4
; Sequence 4, Application US/09079029
; Patent No. 6342369
;  GENERAL INFORMATION:
;    APPLICANT:  Adams, Camilia W.
,    APPLICANT:  Ashkenazi, Avi J.
,    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Kim, Kyung J.
;    TITLE OF INVENTION:  Apo-2 Receptor
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
,      CITY:  South San Francisco
;      STATE:  California
,      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
,      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
,      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
,    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,029
,      FILING DATE:
;      CLASSIFICATION:
,    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Marschang, Diane L.
;       REGISTRATION NUMBER:  35,600
;       REFERENCE/DOCKET NUMBER:  P1052R2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650/225-5416
;       TELEFAX:  650/952-9881
;   INFORMATION FOR SEQ ID NO:  4
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  29 base pairs
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
US-09-079-029-4

  Query Match             100.0%;  Score 25;  DB 4;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-11;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 10
US-08-928-069-14
; Sequence 14, Application US/08928069
; Patent No. 6462176
;  GENERAL INFORMATION:
;    APPLICANT:  Ashkenazi, Avi J.
;    TITLE OF INVENTION:  Apo 3 POLYPEPTIDE
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/928,069
;      FILING DATE:  11-Sep-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/717,843
;      FILING DATE:  09/23/1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marschang, Diane L.
;      REGISTRATION NUMBER:  35,600
;      REFERENCE/DOCKET NUMBER:  P1052R1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5416
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-928-069-14

  Query Match             100.0%;  Score 25;  DB 4;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-12;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 11
US-08-928-683A-10
; Sequence 10, Application US/08928683A
; Patent No. 6469144
;  GENERAL INFORMATION:
;       APPLICANT: Ashkenazi, Avi J.
;       TITLE OF INVENTION: Apo 2 LI AND Apo 3 POLYPEPTIDE
;       NUMBER OF SEQUENCES: 28
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/928,683A
;            FILING DATE: 21-Mar-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/626,328
;            FILING DATE: 1-Apr-1996
;            APPLICATION NUMBER: 08/711,800
;            FILING DATE: 23-Sep-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Marschang, Diane L.
;            REGISTRATION NUMBER: 35,600
;            REFERENCE/DOCKET NUMBER: P1007P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5416
;            TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 29 base pairs
;            TYPE: Nucleic Acid
;            STRANDEDNESS: Single
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-928-683A-10

  Query Match             100.0%;  Score 25;  DB 4;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-12;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 12
US-08-484-997A-25
; Sequence 25, Application US/08484997A
; Patent No. 5969055
;  GENERAL INFORMATION:
;    APPLICANT:  Juan, Shao-Chieh
;    APPLICANT:  Lichenstein, Henri S.
;    APPLICANT:  Wright, Samuel D.
;    TITLE OF INVENTION:  ANTI INFLAMMATORY IL-4 POLYPEPTIDES
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC
;      STREET:  1840 DeHavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-484-397A-25

Query Match 100.0%; Score 25; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
Db 6 AGGGACTTTCCGCTGGGGACTTTCC 30

RESULT 13
US-08-484-397A-26/c
; Sequence 26, Application US/08484397A
; Patent No. 5869455
; GENERAL INFORMATION:
; APPLICANT: Juan, Shao-Chieh
; APPLICANT: Lichenstein, Henri S.
; APPLICANT: Wright, Samuel D.
; TITLE OF INVENTION: ANTI-INFLAMMATORY C3/4 POLYPEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,397A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-484-397A-26

Query Match 100.0%; Score 25; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
Db 32 AGGGACTTTCCGCTGGGGACTTTCC 8

RESULT 14
US-08-465-590-142
; Sequence 142, Application US/08465590
; Patent No. 5824770
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUCETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AscII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,590
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,439
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MFG 0000LDV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-465-590-142

Query Match 100.0%; Score 25; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
Db 3 AGGGACTTTCCGCTGGGGACTTTCC 27

RESULT 15
US-08-711-417C-142
; Sequence 142, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:

; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: [illegible]
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-08-711-417C-142

Query Match 100.0%; Score 25; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 3 AGGGACTTTCCGCTGGGGACTTTCC 27

Search completed: December 1, 2002, 07:36:03
Job time : 53 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 16:26:42 ; Search time 267 Seconds
(without alignments)
210.861 Million cell updates/sec

Title: US-09-844-915-1
Perfect score: 25
Sequence: 1 aaggctttccgctggggactttcc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185230 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370459

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1985.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1983.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1984.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1982.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn.embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	25	100.0	25	24	ABL58384	NF kappaB binding
2	25	100.0	25	24	ABL58385	NF kappaB binding
3	25	100.0	27	11	AAQ04699	HIV enhancer negat
4	25	100.0	27	17	AAT40192	HIV target sequenc
5	25	100.0	27	17	AAT30587	Target binding reg
6	25	100.0	27	17	AAT31196	Target binding reg
7	25	100.0	28	15	AAQ74525	Primer for the amp
8	25	100.0	28	15	AAQ74616	Primer for the amp
9	25	100.0	29	15	AAQ73477	NF KB transcriptio
10	25	100.0	29	20	AAX59847	NF kappaB specific
11	25	100.0	29	20	AAX59855	NF kappaB specific
12	25	100.0	29	20	AAY84353	Human NF kappa B o
13	25	100.0	29	20	AAV72528	NF kappaB specific
14	25	100.0	29	22	AAH24297	NF kappa B EMSA pr
15	25	100.0	29	22	AAF84483	NF-kappa B electro
16	25	100.0	29	24	ABL41731	Nucleotide sequenc
17	25	100.0	30	22	AAD17455	Nuclear factor kap
18	25	100.0	32	22	AAU17457	Human immunodefici
19	25	100.0	33	20	AAX24336	HIV probe correspon
20	25	100.0	34	10	AAN90922	Part of the kappa
21	25	100.0	34	22	AAC66959	Lymphoid cell nucl
22	25	100.0	36	19	AAV67098	HIV LTR #2. Human
23	25	100.0	37	15	AAQ61844	HIV long termina
24	25	100.0	37	15	AAQ73476	NF KB transcripti
25	25	100.0	37	17	AAT30615	Probe nucleic acid
26	25	100.0	37	19	AAV45402	HIV LTR binding s
27	25	100.0	44	17	AAT30604	Target binding reg
28	25	100.0	44	17	AAT30605	Target binding reg
29	25	100.0	44	21	AAZ44474	HIV LTR NF kB clo
30	25	100.0	44	21	AAL42151	HIV Lta NFkappaB t
31	25	100.0	45	17	AAT30603	Target binding reg
32	25	100.0	45	17	AAT30606	Target binding reg
33	25	100.0	45	17	AAT30599	Target binding reg
34	25	100.0	45	20	AAX28079	HIV-LTR oligonucle
35	25	100.0	46	17	AAT30607	Target binding reg
36	25	100.0	46	17	AAT30600	Target binding reg
37	25	100.0	46	17	AAT30601	Target binding reg
38	25	100.0	46	17	AAT30602	Target binding reg
39	25	100.0	54	16	AAQ84607	Human immunodefici
40	25	100.0	54	17	AAT18552	Human immunodefici
41	25	100.0	54	21	AAX21112	HIV region I prime
42	25	100.0	55	17	AAT31612	Target binding reg
43	25	100.0	70	17	AAT30614	Target binding reg
44	25	100.0	72	17	AAT30617	Probe nucleic acid
45	25	100.0	92	21	AAL42154	HIV 1 LTR Spl bind

ALIGNMENTS

RESULT 1
ABL58384
ID ABL58384 standard; DNA; 25 BP.
XX
AC ABL58384;
XX
DT 31-MAY-2002 (first entry)
XX
DE NF kappaB binding sites containing redox ODN.
XX
KW inflammation, dendritic, nuclear factor, NF kappaB; antidiabetic;
KW antiarthritic, immunosuppressive; antiasthmatic; antibacterial;
KW nephrotropic, antiatherosclerotic, anti HIV, ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 2..11
FT /*tag= a
FT /note= "NF-kappaB binding site"
FT misc_feature 16..25
FT /*tag= b
FT /note= "NF-kappaB binding site"
XX
PN WO0301383713 A2.
XX
PD 09-NOV-2001.
XX
PF 31-MAY-2001; 2001WO-US015661.
XX
PR 28-APR-2000; 2000US-200479P.
XX

PA (UYPI) UNIV PITTSBURGH.
XX
PI Robbins PD, Lu L, Giannoukakis N;
XX
DR WPI; 2002-034509/04.
XX
PT Tolerogenic dendritic cell, useful for enhancing tolerogenicity in
PT mammalian host and treating asthma and septic shock, comprises
PT oligodeoxyribonucleotide having one or more nuclear factor kappaB
PT binding sites
XX
PS Claim 3, Page 17; 64pp; English.
XX
CC The invention relates to a tolerogenic dendritic cell (I) comprising an
CC oligodeoxyribonucleotide (ODN) having one or more nuclear factor (NF)-
CC kappaB binding sites. (I) is useful for enhancing tolerogenicity in a
CC mammalian host, (a transplant host or a host having Type I diabetes or an
CC inflammatory related disease such as arthritis). The method involves
CC preparing (I) and administering it to the host. The method further
CC involves administering FK506 and/or cyclosporine A to the host. (I) is
CC also useful for treating diabetes. Enhanced tolerogenicity produced by
CC (I) is useful for prolonging foreign graft survival and for ameliorating
CC inflammatory related diseases, such as autoimmune diseases e.g.,
CC autoimmune arthritis, autoimmune diabetes, asthma, septic shock, lung
CC fibrosis, glomerulonephritis, atherosclerosis and AIDS. The present
CC sequence represents an ODN comprising two NF-kappaB binding sites.
XX
SQ Sequence 25 BP; 3 A; 7 C; 8 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 1 AGGGACTTTCCGCTGGGGACTTTCC 25

RESULT 2
ABL58385/c
ID ABL58385 standard; DNA; 25 BP.
XX
AC ABL58385;
XX
DT 30-JUL-2002 (first entry)
XX
DE NF-kappaB binding sites containing antisense ODN.
XX
KW Tolerogenicity; dendrite; nuclear factor, NF-kappaB; antidiabetic;
KW antiarthritic; immunosuppressive; antiasthmatic; antibacterial;
KW nephrotropic; antiatherosclerotic; anti-HIV; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..10
FT /*tag= a
FT /note= "NF-kappaB binding site"
FT
FT misc_feature 15..24
FT /*tag= b
FT /note= "NF-kappaB binding site"
FT
XX
PN WO200197713-A2.
XX
PD 28-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US13661.
XX
PR 28-APR-2000; 2000US-200479P.
XX
PA (UYPI) UNIV PITTSBURGH.
XX
PI Robbins PD, Lu L, Giannoukakis N;
XX
DR WPI; 2002-034509/04.
XX
PT Tolerogenic dendritic cell, useful for enhancing tolerogenicity in
PT mammalian host and treating asthma and septic shock, comprises
PT oligodeoxyribonucleotide having one or more nuclear factor kappaB
PT binding sites -
XX
PS Example 1; Page 17; 64pp; English.
XX
CC The invention relates to a tolerogenic dendritic cell (I) comprising an
CC oligodeoxyribonucleotide (ODN) having one or more nuclear factor (NF)-
CC kappaB binding sites. (I) is useful for enhancing tolerogenicity in a
CC mammalian host, (a transplant host or a host having Type I diabetes or an
CC inflammatory related disease such as arthritis). The method involves
CC preparing (I) and administering it to the host. The method further
CC involves administering FK506 and/or cyclosporine A to the host. (I) is
CC also useful for treating diabetes. Enhanced tolerogenicity produced by
CC (I) is useful for prolonging foreign graft survival and for ameliorating
CC inflammatory related diseases, such as autoimmune diseases e.g.,
CC autoimmune arthritis, autoimmune diabetes, asthma, septic shock, lung
CC fibrosis, glomerulonephritis, atherosclerosis and AIDS. The present
CC sequence represents an ODN comprising two NF-kappaB binding sites.
XX
SQ Sequence 25 BP; 7 A; 8 C; 7 G; 3 T; 0 other;

Query Match 100.0%; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 25 AGGGACTTTCCGCTGGGGACTTTCC 1

RESULT 3
AAQ04699
ID AAQ04699 standard; DNA; 27 BP.
XX
AC AAQ04699;
XX
DT 11-OCT-1990 (first entry)
XX
DE HIV enhancer negative element.
XX
OS Homo sapiens
XX
KW HIV; AIDS; beta-interferon; promoter; islet cells; gastrin; ds.
XX
PN WO9005146-A.
XX
PD 17-MAY-1990.
XX
PF 31-OCT-1989; 89WO-0004877.
XX
PR 31-OCT-1988; 88US-0265385.
XX
PA (GEHO-) GEN HOSPITAL CORP.
XX
PI Brand SJ;
XX
DR WPI; 1990-178799/23.
XX
PT Purified protein binding to nucleotide sequence -
PT with islet cell specific negative regulatory element of gastrin
PT gene.
XX
PS Disclosure; ; pp; English.
XX
CC Protein binding site is similar to human interferon gene element,
CC and may thus be used to regulate expression of interferon and other
CC genes containing such elements.
CC Protein may be used to inhibit gastrin expression, and thus

CC unwanted development of gastrin dependent islet cells in islet
CC tumours and neonatal hesidioblastosis.
CC see also AAQ04499.
XX
SQ Sequence 27 BP; 4 A; 8 C; 9 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 11; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
Db 1 AGGGACTTTCCGCTGGGGACTTTCC 25

RESULT 4
AAT40192
ID AAT40192 standard; DNA; 27 BP.
XX
AC AAT40192;
XX
DT 25-APR-1997 (first entry)
XX
DE HIV target sequence #11.
XX
KW HIV; probe; primer; amplify; polymerase chain reaction; microorganism;
KW BCL-2; PCR; hepatitis B virus; HBV; CML; ss.
XX
OS Human immunodeficiency virus type 1.
XX
PN EP731175-A2.
XX
PD 11-SEP-1996.
XX
PF 10-JUL-1990; 90EP-0307503.
XX
PR 11-JUL-1989; 89US-0378501.
XX
PA (GENP) GEN-PROBE INC.
XX
PI McDonough S;
XX
DR WPI; 1996-403335/41.
XX
PT Detection of HIV nucleic acids in samples - using new specific
PT oligonucleotide(s) for the amplification and detection of target
PT sequences.
XX
PS Claim 1; Page 70; 95pp; English.
XX
CC AAT40182 (40131, and AAT42414 (42414 represent HIV target sequences.
CC These sequences (which may be represented by AAT42414-T42415) can be used as
CC probes for HIV, or as primers for specific regions of the HIV genome.
CC These sequences can be used in kits of the invention, for detecting the
CC presence of HIV nucleic acid sequences in a sample. The kits comprise
CC two amplification primers (such as AAT40182 and AAT40192), and a probe
CC (such as AAT42404) for detection of the amplified sequence. By using
CC these sequences, the amplification of HIV nucleic acid sequences is
CC improved. The kits can also be used for the detection of other
CC microorganisms, by using different probe sequences. Other sequences that
CC can be detected using this method include those from BCL-2 (using the
CC sequences shown in AAT42413 T42414), hepatitis B virus (using
CC AAT42410 T42411), and CML (using AAT42417 T42418). The samples can be
CC clinical, environmental or forensic samples, and the method produces
CC large amounts of the target sequence for a variety of uses. The method
CC can also be used to produce multiple copies of a target sequence for use
CC in cloning, and sequencing, and to produce probes for the target
CC sequence.
XX
SQ Sequence 27 BP; 4 A; 8 C; 8 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
Db 1 AGGGACTTTCCGCTGGGGACTTTCC 27

RESULT 5
AAT30587
ID AAT30587 standard; DNA; 27 BP.
XX
AC AAT30587;
XX
DT 19-FEB-1997 (first entry)
XX
DE Target binding region #7.
XX
KW Target binding assembly; nucleic acid recognition unit; NF kappa B; SP1;
KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
KW virus; ss.
XX
OS Synthetic.
XX
PN WO9617956-A2.
XX
PD 13-JUN-1996.
XX
PF 07-DEC-1995; 95WO-US15944.
XX
PR 09-DEC-1994; 94US-00353476.
XX
PA (GENE-) GENE POOL INC.
XX
PI Weininger AM, Weininger S;
XX
DR WPI; 1996-287199/29.
XX
PT Probe nucleic acids, target binding assemblies, etc. for detection
PT and localisation of specific nucleic acid sequences, esp. HIV and
PT HPV
XX
PS Disclosure; Page 66; 172pp; English.
XX
CC AAT30581-T30614 represent target binding regions (TBR) of a probe of the
CC invention. The probe of the invention contains a TBR, a booster binding
CC region (BBR), and an optional support or attachment (OSA). The target
CC binding assembly (TBA) recognised by the probe, contains at least one
CC nucleic acid recognition unit (NAU), and optionally a linker sequence,
CC an assembly sequence (see AAP30594-P30595), an asymmetry sequence (see
CC AAP36333-P36360), a nuclear localisation signal sequence (see AAP96007),
CC and an OSA. The assembly sequence and asymmetry sequence are
CC responsible for the folding and association of the NAUs. The NAUs (see
CC AAP30581-P30593) are selected from NF-kappa-B, SP1, TATA, human
CC papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR
CC and Tat binding units. The linker sequence is an oligopeptide, which
CC does not interfere with NAU function, but provides stability and control
CC over the spacing of the NAU from the rest of the TBA. The OSA is an
CC attached support or indicator, or other means of localisation of the
CC probe. The probe can be used in a method for detection or localisation a
CC specific target nucleic acid sequence (TNA). The method is highly
CC sensitive, and has a high degree of specificity. The method can be used
CC for detecting specific nucleic acid sequences, including those found in
CC human cells, in HIV, HPV, and other nucleic acid containing systems,
CC including bacteria and viruses.
XX
SQ Sequence 27 BP; 5 A; 7 C; 8 G; 7 T; 0 other;

Query Match 100.0%; Score 25; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           ||||||||||||||||||||||||||
Db       2 AGGGACTTTCCGCTGGGGACTTTCC 26
```

```
RESULT 6
AAT30588
ID   AAT30588 standard; DNA; 27 BP.
XX
AC   AAT30588;
XX
DT   19-FEB-1997  (first entry)
XX
DE   Target binding region #8.
XX
KW   Target binding assembly, nucleic acid recognition unit, NF-kappa-B; SP1;
KW   TATA, human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
KW   HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
KW   nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
KW   virus; ss
XX
OS   Synthetic.
XX
PN   WO9617956-A2.
XX
PD   13-JUN-1996.
XX
PF   07-DEC-1995;   95WO-US15944.
XX
PR   09-DEC-1994;   94US-0353476.
XX
PA   (GENE-) GENE POOL INC.
XX
PI   Weininger AM,  Weininger S;
XX
DR   WPI; 1996-287199/29.
XX
PT   Probe nucleic acids, target binding assemblies, etc - for detection
PT   and localisation of specific nucleic acid sequences, esp. HIV and
PT   HPV
XX
PS   Disclosure; Page 66; 172pp; English.
XX
CC   AAT30581-T30614 represent target binding regions (TBR) of a probe of the
CC   invention. The probe of the invention contains a TBR, a booster binding
CC   region (BBR), and an optional support or attachment (OSA). The target
CC   binding assembly (TBA) recognised by the probe, contains at least one
CC   nucleic acid recognition unit (NAR), and optionally a linker sequence,
CC   an asymmetry sequence (see AAR95994-R96004), an asymmetry sequence (see
CC   AAR95999-R96009), a nuclear localisation signal sequence (see AAP96007-
CC   AAR96065-R96093) are selected from NF-kappa B, SP1, TATA, human
CC   papillomavirus (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR
CC   and Tat binding units. The linker sequence is an oligopeptide, which
CC   does not interfere with NAR function, but provides stability and control
CC   over the spacing of the NAR from the rest of the TBA. The OSA is an
CC   attached support or indicator, or other means of localisation of the
CC   probe. The probe can be used in a method for detecting or localising a
CC   specific target nucleic acid sequence (TNA). The metnod is highly
CC   sensitive, and has a high degree of specificity. The method can be used
CC   for detecting specific nucleic acid sequences, including those found in
CC   human cells, in HIV, HPV, and other nucleic acid containing systems,
CC   including bacteria and viruses.
XX
SQ   Sequence 27 BP; 4 A; 7 C; 9 G; 7 T; 0 other;

  Query Match          100.0%;  Score 25;  DB 17;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 0.047;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       2 AGGGACTTTCCGCTGGGGACTTTCC 26
```

```
RESULT 7
AAQ74525
ID   AAQ74525 standard; DNA; 28 BP.
XX
AC   AAQ74525;
XX
DT   04-MAY-1995  (first entry)
XX
DE   Primer for the amplification of HIV-1 sequences.
XX
KW   Probe; primer; detection; amplification; identification; diagnosis;
KW   HIV-1; human immunodeficiency virus, HTLV-1; AIDS;
KW   human T-cell leukaemia virus; acquired immune deficiency syndrome;
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag= a
FT                   /note= "N may be absent or is a 5' oligonucleotide
FT                   sequence which is specifically recognised by
FT                   an enzyme, e.g. the promoter sequence for T7,
FT                   T3 or SP6 RNA polymerase, which enhances
FT                   initiation or elongation of RNA transcription
FT                   by an RNA polymerase.  The sequence may be
FT                   e.g. 5'-AATTTAATACGACTCACTATAGGGAGA-3'"
FT
XX
PN   EP617132-A.
XX
PD   28-SEP-1994.
XX
PF   28-MAR-1994;   94EP-0302196.
XX
PR   26-MAR-1993;   93US-0040745.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Mcdonough SH,  Ryder TB,  Yang Y;
XX
DR   WPI; 1994-295780/37.
XX
PT   New oligonucleotides corresponding to HIV-1 sequences - used for
PT   selective amplification and as hybridisation probes for detection
PT   of HIV-1.
XX
PS   Claim 9; Page 4, 69pp; English.
XX
CC   Probes and primers specific for HIV 1 were identified by comparison
CC   of published sequences of HIV-1, HIV-2, HTLV-1 and HTLV-2 and were
CC   then synthesised. The primers can be used for the selective
CC   amplification of HIV-1 nucleic acid in a sample and may therefore be
CC   useful in detection methods.  See AAQ74500 74532.
XX
SQ   Sequence 28 BP; 4 A; 8 C; 8 G; 7 T; 1 other;

  Query Match          100.0%;  Score 25;  DB 15;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 0.048;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 8
AAQ74616
ID   AAQ74616 standard; RNA; 28 BP.
XX
AC   AAQ74616;
```

```
XX
DT   05-MAY-1995  (first entry)
XX
DE   Primer for the amplification of HIV-1 sequences.
XX
KW   Probe, primer, detection, amplification, identification, diagnosis,
KW   HIV 1, human immunodeficiency virus, HTLV I, AIDS,
KW   human T-cell leukaemia virus; acquired immune deficiency syndrome,
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag= a
FT                   /note= "N may be absent or is a 5' oligonucleotide
FT                   sequence which is specifically recognised by
FT                   an enzyme, e.g. the promoter sequence for T7,
FT                   T3 or SP6 RNA polymerase, which enhances
FT                   initiation or elongation of RNA transcription
FT                   by an RNA polymerase.  The sequence may be
FT                   e.g. 5'-AATTTAATACGACTCACTATAGGGAGA-3'"
XX
PN   EP617130-A.
XX
PD   28-SEP-1994
XX
PF   28-MAR-1994;   94EP-0302196
XX
PR   26 MAR 1993;   93US-0036946
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Mcdonough SH,  Ryder TB,  Yang Y;
XX
DR   WPI; 1994-295780/36.
XX
PT   New oligonucleotides corresponding to HIV 1 sequences - used for
PT   selective amplification and as hybridisation probes for detection
PT   of HIV-1.
XX
PS   Claim 3; Page 56; 69pp; English.
XX
CC   Probes and primers specific for HIV 1 were identified by comparison
CC   of published sequences of HIV 1, HIV 2, HTLV 1 and HTLV 2 and were
CC   then synthesised. The primers can be used for the selective
CC   amplification of HIV-1 nucleic acid in a sample and may therefore be
CC   useful in detection methods.  See AAQ74500-74533 and AAQ74691-674693
XX
SQ   Sequence 28 BP; 4 A; 8 C; 8 G; 7 U; 1 other;

  Query Match             100.0%;  Score 25;  DB 15;  Length 28;
  Best Local Similarity   92.0%;  Pred. No. 0.048;
  Matches   18;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           ||||||||||||||||||||||||| |
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 9
AAQ73477/c
ID   AAQ73477 standard; DNA; 28 BP.
XX
AC   AAQ73477;
XX
DT   12-JUN-1995  (first entry)
XX
DE   NF KB transcription factor binding motif
XX
KW   NF KB, transcription factor, binding motif, antibody, detection,
KW   determination; ss.
XX
OS   Synthetic.
XX
PN   EP620439-A
XX
PD   19-OCT-1994.
XX
PF   08-APR-1994;   94EP-0105557.
XX
PR   16 APR-1993;   93DE-4312399.
XX
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI   Doppler C,  Hinzpeter M,  Stollinger H;
XX
DR   WPI; 1994-318471/40.
XX
PT   Determn. of binding of transcription factor to nucleic acid - by
PT   incubating together, one component immobilised, and reaction with
PT   labelled antibody, to detect activated cells for diagnosis of
PT   cancer and autoimmune disease.
XX
PS   Claim 12; Page 8; 9pp; German.
XX
CC   The binding of the transcription factor (TF) to its binding motif is
CC   determined by: (1) binding the TF or its binding motif to a solid
CC   phase, (2) incubating TF and its binding motif, (3) adding a
CC   labelled antibody specific for TF or its binding motif; if the
CC   antibody is directed against the immobilised reactant then it will
CC   compete with the other reactant for binding, (4) separating the
CC   solid and liquid phases, and (5) determining the amount of label in
CC   one of the phases as a measure of the binding between TF and its
CC   binding motif.
XX
SQ   Sequence 28 BP; 7 A; 9 C; 7 G; 5 T; 0 other;

  Query Match             100.0%;  Score 25;  DB 15;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.048;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db      27 AGGGACTTTCCGCTGGGGACTTTCC 3


RESULT 10
AAX59847
ID   AAX59847 standard; DNA; 29 BP.
XX
AC   AAX59847;
XX
DT   28-JUL-1999  (first entry)
XX
DE   NF-kappaB specific oligonucleotide probe.
XX
KW   DNA10355, tumour necrosis factor homologue; receptor SITP;
KW   immunogen, antibody, apoptosis, carcinoma cancer cell;
KW   tumour necrosis factor (TNF)-alpha secretion, primary T cell;
KW   proinflammatory response; probe; ss.
XX
OS   Synthetic.
XX
PN   WO9925834-A1.
XX
PD   27-MAY-1999.
XX
PF   18-NOV-1998;   98WO-US24621.
XX
PR   12 DEC 1997;   97US-0069661
PR   18-NOV-1997;   97US-0065635
XX
PA   (SOTH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Godowski PJ,  Gurney AL;
```

PI Mark MR, Marsters SA, Pitti R;
XX
DR WPI; 1999-338009/28.
XX
PT New DNA19355 polypeptide
XX
PS Example 5; Page 48; 88pp; English.
XX
CC The present sequence represents a NF-kappaB specific oilgonucleotide
CC probe, used in the course of the invention. The specification describes
CC a novel polypeptide designated DNA19355. The polypeptide is a tumour necrosis
CC factor homologue. The DNA19355 polypeptide sequence can be used to
CC derive hybridisation probes for e.g. isolating similar sequences, gene
CC mapping, genetic analysis, etc. Nucleic acids which encode DNA19355 can
CC also be used to generate transgenic or knockout animals, which are
CC useful in the development and screening of therapeutically useful
CC reagents. The DNA19355 polypeptides may be used in diagnostic assays to
CC detect the presence of the receptor GITR in mammalian tissues. The
CC polypeptides can also be used as immunogens to raise antibodies. The
CC polypeptides may also be used to induce apoptosis in mammalian cancer
CC cells. DNA19355 polypeptides stimulate secretion of tumour necrosis
CC factor (TNF) alpha in primary T- cells, and so can be used to stimulate
CC a proinflammatory response in mammalian cells.
XX
SQ Sequence 29 BP; 4 A; 8 C; 9 G; 8 T; 0 other;

Query Match 100.0%; Score 25; DB 20; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 4 AGGGACTTTCCGCTGGGGACTTTCC 28

RESULT 11
AAX56005
ID AAX56005 standard; DNA; 29 BP.
XX
AC AAX56005;
XX
DT 15-JUL-1999 (first entry)
XX
DE NF-kappaB specific oligonucleotide probe.
XX
KW Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apoptosis;
KW NF-kappaB-dependent transcription; JNK/SAPK-dependent response;
KW cancer; hybridisation; probe; ss.
XX
OS Synthetic.
XX
PN WO9919490-A1.
XX
PD 22-APR-1999.
XX
PF 09-OCT-1998; 98WO-US21407.
XX
PR 17-DEC-1997; 97US-0069862.
PR 10-OCT-1997; 97US-0062047.
XX
PA (GETH) GENENTECH INC
XX
PI Ashkenazi AJ, Marsters SA, Pitti R;
XX
DR WPI; 1999-287997/24.
XX
PT New human Apo-3 ligand (a tumour necrosis factor) homologue
XX
PS Example 4; Page 38; 74pp; English.
XX
CC The present invention describes a human tumour necrosis factor (TNF)
CC and lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has
CC cytostatic activity. Apo-3 ligand can be used to induce apoptosis in
CC mammalian cancer cells, to induce NF-kappaB-dependent transcription and
CC to induce JNK/SAPK-dependent responses in mammalian cells. The present
CC sequence represents an NF-kappaB-specific oligonucleotide probe, which
CC is used in an example from the present invention
XX
SQ Sequence 29 BP; 4 A; 8 C; 9 G; 8 T; 0 other;

Query Match 100.0%; Score 25; DB 20; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 4 AGGGACTTTCCGCTGGGGACTTTCC 28

RESULT 12
AAV84353
ID AAV84353 standard; DNA; 29 BP.
XX
AC AAV84353;
XX
DT 26-APR-1999 (first entry)
XX
DE Human NF kappa B oligonucleotide probe.
XX
KW NF kappa B; Apo-2DcR; human; tumour necrosis factor receptor;
KW neurodegeneration; autoimmune disease; inflammation; cancer;
KW apoptosis; therapy; probe; Apo-2 ligand; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9858062-A1.
XX
PD 23-DEC-1998.
XX
PF 12-JUN-1998; 98WO-US12456.
XX
PR 18-JUN-1997; 97US-0878168.
XX
PA (GETH) GENENTECH INC
XX
PI Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;
PI Kim KJ, Wood WI;
XX
DR WPI; 1999-095540/08.
XX
PT New Apo 2DcR polypeptide used for modulation and diagnosis of
PT apoptosis, e.g. in neurodegeneration
XX
PS Example 10; Page 44; 88pp; English.
XX
CC This synthetic oligonucleotide is used as a probe for NF-kappa B
CC nucleotide sequences. It was used in experiments to demonstrate
CC activation of NF-kappa B by Apo-2 ligand (see AAW88410). The
CC invention relates to Apo-2DcR (see AAW88408), a novel member of the
CC tumour necrosis factor receptor family that binds to Apo-2 ligand
CC and is involved in apoptosis. Apo-2DcR polypeptides are used to
CC modulate apoptosis of mammalian cells (claimed) e.g. in the
CC treatment of neurodegeneration, autoimmune diseases and
CC inflammation. The Apo-2DcR polypeptides are optionally used in
CC conjunction with Apo-2 ligand, the bioavailability of which is
CC increased by antibody-mediated blockade of Apo-2DcR.
XX
SQ Sequence 29 BP; 4 A; 8 C; 9 G; 8 T; 0 other;

Query Match 100.0%; Score 25; DB 20; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||

Db 4 AGGGACTTTCCGCTGGGGACTTTCC 28

RESULT 13
AAV72528
ID AAV72528 standard; DNA; 29 BP.
XX
AC AAV72528;
XX
DT 16-MAR 1999 (first entry)
XX
DE NF KappaB specific oligonucleotide probe #1.
XX
KW Human; Apo 2, receptor, apoptosis, neurodegenerative disease, cancer,
KW tumour necrosis factor, TNF, tumour necrosis factor receptor, TNFR,
KW TNF cytokine; probe; hybridisation; ss.
XX
OS Synthetic.
OS Homo sapiens
XX
PN WO9851793-A1.
XX
PD 19-NOV 1998.
XX
PF 14-MAY 1998; 98WO-US009704.
XX
PR 09-FEB 1998; 98US-0020746.
PR 15-MAY 1997; 97US-0857216.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX
DR WPI; 1999-045228/04.
XX
PT Human Apo 2 polypeptide inducing apoptosis - useful to treat
PT conditions linked with decreased apoptosis e.g. cancer, and produce
PT antibodies to increase or decrease apoptosis
XX
PS Example 6; Page 69; 131pp; English.
XX
CC The present invention describes human Apo 2. Apo 2 can be used
CC therapeutically to induce apoptosis in mammalian cells, and is useful
CC to treat conditions associated with decreased apoptosis e.g. cancer.
CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
CC binding to TNFRs, and Apo 2 triggered caspase-dependent apoptosis. It
CC can be used to identify agents activating Apo 2, useful to treat
CC mammalian cancer cells, and to produce Apo 2 chimeras useful
CC therapeutically (e.g. those containing immunoglobulin sequences can be
CC inhibit apoptosis) or diagnostically (e.g. the surprising in epitope
CC tag polypeptide allow Apo 2 detection and purification using anti-tag
CC antibodies). It can be used to produce antibodies which can be combined
CC with a (particularly pharmaceutically acceptable) carrier in compositions
CC or used to produce dimeric molecules (especially homodimeric Fc-Apo
CC comprising first and second Apo-2 antibodies). Agonistic (especially
CC single-chain) antibodies can be administered to induce apoptosis in
CC mammalian cancer cells, and antagonistic antibodies used to block
CC endogenous apoptosis (e.g. in neurodegenerative diseases). Apo 2
CC antibodies can also be used diagnostically e.g. to screen Apo 2
CC expression in cells/tissues and in Apo 2 purification. The present
CC sequence represents an NF-kappaB-specific oligonucleotide probe from an
CC example of the present invention
XX
SQ Sequence 29 BP; 4 A; 9 C; 9 G; 6 T; 1 other;

Query Match 100.0%; Score 29; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
Db 4 AGGGACTTTCCGCTGGGGACTTTCC 28

RESULT 14
AAH24297
ID AAH24297 standard; DNA; 29 BP.
XX
AC AAH24297;
XX
DT 21-SEP-2001 (first entry)
XX
DE NF kappa B EMSA probe.
XX
KW NF kappa B inhibition; nuclear factor kappa-B; GSK-3 inhibitor;
KW glycogen synthase kinase 3; hyperproliferative disorder; cancer;
KW inflammatory disorder; autoimmune disorder; asthma;
KW type I diabetes mellitus; myasthenia gravis; Grave's disease;
KW rheumatoid arthritis; allograft rejection; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; multiple sclerosis; psoriasis;
KW systemic lupus erythematosus; SLE; glomerulonephritis; scleroderma;
KW vasculitis; inflammatory autoimmune myositis; autoimmune thyroiditis;
KW contact dermatitis; rhinitis; allergy; septic shock; systemic shock;
KW lung fibrosis; atherosclerosis; AIDS;
KW electrophoretic mobility shift assay, EMSA probe; ds.
XX
OS Synthetic.
XX
PN WO200147533-A2.
XX
PD 05-JUL-2001.
XX
PF 21-DEC-2000; 2000WO-CA01578.
XX
PR 23-DEC-1999; 99US-0172364.
XX
PA (ONTA) ONTARIO CANCER INST.
XX
PI Hoeflich K, Luo J, Woodgett J;
XX
DR WPI; 2001-418157/44.
XX
PT Inhibiting nuclear factor-kappa-B activity in a cell for treating
PT asthma, lupus, scleroderma, cancer, psoriasis, inflammation, comprises
PT contacting the cell with an inhibitor of glycogen synthase kinase 3 -
XX
PS Example 4; Page 21; 39pp; English.
XX
CC The invention relates to a method of inhibiting the activity of nuclear
CC factor kappa-B (NF kappa-B) in a cell via the use of an inhibitor of
CC glycogen synthase kinase 3 (GSK 3 -). In particular NF kappa B activity is
CC reduced by decreasing the activity of the beta isoform of GSK 3 - (GSK 3b-).
CC Inappropriate activation of NF kappa B is associated with inflammatory
CC and hyperproliferative disorders. GSK 3 inhibitors suitable for use
CC in the method of the invention include lithium, valproic acid,
CC granulatimide-, bisindolylmaleimides, anti-GSK-3 antibodies and GSK-3 antisense
CC oligonucleotides as well as agents which indirectly inhibit GSK 3,
CC such as wortmannin and staurosporine. The invention also encompasses
CC methods of screening for modulators of GSK-3b function, and a transgenic
CC transgenic animal which has a defect in GSK 3 function for use as a
CC model for GSK 3 function. The invention additionally encompasses methods
CC for the enhanced killing of tumour cells through the sensitisation
CC action of GSK 3 inhibition, when GSK 3 inhibitors are administered in
CC conjunction with apoptosis-inducing ligands of TNFR1 (tumour necrosis
CC factor receptor 1). Such methods are useful for treating
CC hyperproliferative disorders such as cancer and psoriasis. The use of
CC GSK 3 inhibitors to inhibit NF kappa B function has applications in the
CC treatment of inflammatory and autoimmune disorders. The conditions that
CC may be treated using the method of the invention include asthma, type I
CC diabetes mellitus, myasthenia gravis, Grave's disease, rheumatoid
CC arthritis, allograft rejection, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, multiple sclerosis, psoriasis, systemic
CC lupus erythematosus (SLE), glomerulonephritis, scleroderma, various
CC forms of vasculitis, inflammatory autoimmune myositis, autoimmune
CC thyroiditis, contact dermatitis, rhinitis, allergies, septic shock,

CC systemic shock, lung fibrosis, atherosclerosis and AIDS. The present
CC sequence is an EMSA (electrophoretic mobility shift assay) probe
CC containing two tandem NF-kappa-B binding sites used to detect
CC NF-kappa-B activation in embryonic stem cells treated with
CC GSK-3b inhibitors.
XX
SQ Sequence 29 BP; 4 A; 8 C; 9 G; 8 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 4 AGGGACTTTCCGCTGGGGACTTTCC 28

RESULT 15
AAF84483
ID AAF84483 standard; cDNA; 29 BP.
XX
AC AAF84483;
XX
DT 25-JUN-2001 (first entry)
XX
DE NF kappa-B electrophoretic mobility shift assay (EMSA) probe
XX
KW Human Apo-2 receptor; caspase-dependent apoptosis induction;
KW programmed cell death; pro-apoptotic; death domain;
KW agonistic antibody; nuclear factor kappa B;
KW NF kappa B activation; cancer; tumour; lung cancer;
KW colon cancer; glioma; electrophoretic mobility shift assay;
KW EMSA probe; ds.
XX
OS Homo sapiens.
XX
PN WO200119861-A2.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US25436.
XX
PR 15-SEP-1999; 99US-0396710.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Chuntherapai A, Kim KJ;
XX
DR WPI; 2001-266005/27.
XX
PT Inducing apoptosis in mammalian cells for treating cancer, comprises
PT exposing mammalian cells or cancer cells expressing Apo-2 receptor, to
PT Apo-2 agonist antibody
XX
PS Example 6; Page 53; 90pp; English.
XX
CC The invention relates to a method for inducing apoptosis in mammalian
CC cells which express the Apo-2 receptor protein (AAB73442, AAB73443).
CC The method involves exposing the cells to an Apo-2 agonistic antibody,
CC which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor
CC (also referred to simply as Apo-2) is a member of the tumour
CC necrosis factor receptor (TNFR) family, and its natural ligand is the
CC Apo-2 ligand (Apo-2L, also known as TRAIL). The Apo-2 receptor is able
CC to trigger caspase-dependent apoptosis, and is also able to activate
CC NF-kappa-B (nuclear factor kappa B). The Apo-2 receptor is an
CC approximately 47 kD type I transmembrane protein, and contains a death
CC domain in the cytoplasmic region (residues 324-392). It exhibits
CC significantly more sequence identity to the apoptosis-linked receptor
CC DR4, which also binds Apo-2L, than other apoptosis-associated proteins.
CC The Apo-2 receptor agonist monoclonal antibodies used in the method of
CC the invention are 4F11.39.7, 3H3.14, 5, 3D5.1.10 and 3H1.18.10. The
CC method of the invention is used to induce apoptosis in Apo-2-expressing
CC cells, particularly cancer cells. It may therefore be used for treating
CC mammalian cancers, especially lung cancer, colon cancer and glioma.
CC The present sequence represents an NF-kappa-B electrophoretic mobility
CC shift assay (EMSA) probe used in an experiment which demonstrated that
CC the Apo-2 receptor was able to activate NF kappa-B.
XX
SQ Sequence 29 BP; 4 A; 8 C; 9 G; 8 T; 0 other;

Query Match 100.0%; Score 25; DB 22; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 4 AGGGACTTTCCGCTGGGGACTTTCC 28

Search completed: December 1, 2002, 07:34:52
Job time : 270 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 06:55:37 ; Search time 2705 Seconds
(without alignments)
268.972 Million cell updates/sec

Title: US 09-844-915-1
Perfect score: 25
Sequence: 1 agggacttccgctgggagcttccc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1465140287 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	% Query Match	Length	DB	ID	Description
1	25	100.0	25	6	AX299019	AX299019 Sequence
2	25	100.0	27	6	AX299022	AX299022 Sequence
3	25	100.0	27	6	AR026200	AR026200 Sequence
4	25	100.0	27	6	AR026280	AR026280 Sequence
5	25	100.0	27	6	AR035435	AR035435 Sequence
6	25	100.0	27	6	AR035436	AR035436 Sequence
7	25	100.0	27	6	E61343	E61343 Probe for d
8	25	100.0	27	6	I82942	I82942 Sequence 44
9	25	100.0	27	6	I83022	I83022 Sequence 12
c 10	25	100.0	28	6	A40180	A40180 Sequence 2
11	25	100.0	29	6	AR.83747	AR083747 Sequence
12	25	100.0	29	6	AX09[illegible]6n	AX[illegible] Sequence
13	25	100.0	29	6	AX[illegible]	AX[illegible] Sequence
c 14	25	100.0	29	6	AX188649	AX188649 Sequence
15	25	100.0	33	6	AR032342	AR032342 Sequence
c 16	25	100.0	33	6	AR032343	AR032343 Sequence
17	25	100.0	34	6	I09458	I09458 Sequence 2
18	25	100.0	36	6	AR049839	AR049839 Sequence
19	25	100.0	36	6	AR149733	AR149733 Sequence
20	25	100.0	37	6	A40179	A40179 Sequence 1
21	25	100.0	37	6	AR035466	AR035466 Sequence
22	25	100.0	44	6	AR035452	AR035452 Sequence
23	25	100.0	44	6	AR035453	AR035453 Sequence
24	25	100.0	45	6	AR027239	AR027239 Sequence
25	25	100.0	45	6	AR035447	AR035447 Sequence
26	25	100.0	45	6	AR035451	AR035451 Sequence
27	25	100.0	45	6	AR035454	AR035454 Sequence
28	25	100.0	46	6	AR035448	AR035448 Sequence
29	25	100.0	46	6	AR035449	AR035449 Sequence
30	25	100.0	46	6	AR035450	AR035450 Sequence
31	25	100.0	46	6	AR035455	AR035455 Sequence
32	25	100.0	54	6	E61328	E61328 Probe for i
33	25	100.0	59	6	AR035460	AR035460 Sequence
34	25	100.0	70	6	AR035462	AR035462 Sequence
35	25	100.0	70	6	AR035465	AR035465 Sequence
36	25	100.0	72	6	AR055681	AR055681 Sequence
37	25	100.0	80	14	HIVLTRCAT	M69075 Human immun
38	25	100.0	86	14	S52561	S52561 /long term
39	25	100.0	103	6	AR035468	AR035468 Sequence
40	25	100.0	128	14	HIV1U15071	U15071 Human immun
41	25	100.0	141	14	HIV1U15068	U15068 Human immun
42	25	100.0	180	14	HIVCBLAA	M63474 Human immun
43	25	100.0	186	14	AF272007	AF272007 HIV-1 isc
44	25	100.0	197	14	AF272009	AF272009 HIV-1 isc
45	25	100.0	220	14	HIVNE020	M58192 Human immun

ALIGNMENTS

RESULT 1
AX299019
LOCUS AX299019 25 bp DNA linear PAT 26-NOV-2
DEFINITION Sequence 1 from Patent WO0183713.
ACCESSION AX299019
VERSION AX299019.1 GI:17129009
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE 1
AUTHORS Robbins,P.D., Lu,L. and Giannoukakis,N.
TITLE The use of tolerogenic dendritic cells for enhancing tolera
in a host and methods for making the same
JOURNAL Patent: WO 0183713 A 1 08-NOV-2001;

UNIV PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/db_xref="taxon:32630"
/note "Synthesized nucleotide sequence"
BASE COUNT 3 a 7 c 8 g 7 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 1 AGGGACTTTCCGCTGGGGACTTTCC 25

RESULT 3
AX299020
LOCUS AX299020 25 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 1 from patent WO0185715.
ACCESSION AX299020
VERSION AX299020.1 GI:17129610
KEYWORDS .
SOURCE synthetic construct.
ORGANISM Synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Robbins,P.D., Lu,L. and Giannoukakis,N.
TITLE The use of tolerogenic dendritic cells for enhancing tolerogenicity in a host and methods for making the same
JOURNAL Patent: WO 0185715 A 2 08-NOV-2001;
UNIV PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthesized nucleotide sequence"
BASE COUNT 7 a 8 c 7 g 3 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 25 AGGGACTTTCCGCTGGGGACTTTCC 1

RESULT 3
AR026200
LOCUS AR026200 27 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 44 from patent US 5856088.
ACCESSION AR026200
VERSION AR026200.1 GI:5937040
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS McDonough,S.H., Ryder,T.B. and Yang,Y.
TITLE Detection of human immunodeficiency virus type 1
JOURNAL Patent: US 5856088-A 44 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"
BASE COUNT 4 a 8 c 8 g 7 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 3 AGGGACTTTCCGCTGGGGACTTTCC 27

RESULT 4
AR026280
LOCUS AR026280 27 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 124 from patent US 5856088.
ACCESSION AR026280
VERSION AR026280.1 GI:5937120
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS McDonough,S.H., Ryder,T.B. and Yang,Y.
TITLE Detection of human immunodeficiency virus type 1
JOURNAL Patent: US 5856088-A 124 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"
BASE COUNT 4 a 8 c 8 g 7 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 3 AGGGACTTTCCGCTGGGGACTTTCC 27

RESULT 5
AR035435
LOCUS AR035435 27 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5871902.
ACCESSION AR035435
VERSION AR035435.1 GI:5952103
KEYWORDS .
SOURCE Unknown
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Weininger,S. and Weininger,A.M.
TITLE Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids
JOURNAL Patent: US 5871902 A 7 16-FEB-1999;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"
BASE COUNT 5 a 7 c 8 g 7 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGACTTTCCGCTGGGGACTTTCC 25
||||||||||||||||||||||||||
Db 2 AGGGACTTTCCGCTGGGGACTTTCC 26

RESULT 6
AR035436
LOCUS AR035436 27 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5871902.
ACCESSION AR035436
VERSION AR035436.1 GI:5952104

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Weiminger,S. and Weiminger,A.M.
  TITLE     Sequence specific detection of nucleic acid hybrids using a
            DNA-binding miniprotein, capable of discriminating perfect
            hybrids from non-perfect hybrids
  JOURNAL   Patent: US 5871922-A 9 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1..27
                     /organism="unknown"
BASE COUNT        4 a      7 c      9 g      7 t
ORIGIN

  Query Match             100.0%;  Score 25;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       2 AGGGACTTTCCGCTGGGGACTTTCC 26


RESULT 7
E61343
LOCUS       E61343                    27 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Probe for detecting oligonucleotide.
ACCESSION   E61343
VERSION     E61343.1  GI:13025905
KEYWORDS    JP 1999046778-A/17.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Daniel,L.K. and Timothy,J.F.
  TITLE     Probe for detecting oligonucleotide
  JOURNAL   Patent: JP 1999046778-A 17 23-FEB-1999;
            GEN-PROBE INC
COMMENT     OS   Artificial Sequence
            PN   JP 1999046778 A/17
            PD   23 FEB-1999
            PF   14 JAN 1998 JP 1998005607
            PP   11 JUL-1989 US        379501
            PI   DANIEL LOUIS KASHIAN,TIMOTHY J PUPUTSU
            PT   "C12N15/09,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1..27
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1..27
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        4 a      8 c      8 g      7 t
ORIGIN

  Query Match             100.0%;  Score 25;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       3 AGGGACTTTCCGCTGGGGACTTTCC 27


RESULT 9
I82942
LOCUS       I82942                    27 bp    DNA     linear   PAT 15-JUN-1998
DEFINITION  Sequence 44 from patent US 5712385.
ACCESSION   I82942
VERSION     I82942.1  GI:3211239
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McDonough,S.H., Ryder,T.B. and Yang,Y.
  TITLE     Detection of human immunodeficiency virus type 1
  JOURNAL   Patent: US 5712385-A 44 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1..27
                     /organism="unknown"
BASE COUNT        4 a      8 c      8 g      7 t
ORIGIN

  Query Match             100.0%;  Score 25;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       3 AGGGACTTTCCGCTGGGGACTTTCC 27


RESULT 10
A40180/c
LOCUS       A40180                    28 bp    DNA     linear   PAT 19-MAR-1997
DEFINITION  Sequence 2 from Patent EP0620439.
ACCESSION   A40180
VERSION     A40180.1  GI:2296331
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Doppler,C.D., Hinzpeter,M.D. and Stockinger,H.D.
  TITLE     Method of determining the binding of transcription factors to
            nucleic acids
  JOURNAL   Patent: EP 0620439-A 2 19-OCT-1994;
            BOEHRINGER MANNHEIM GMBH (DE)
COMMENT     Other publication DE 4312399 941020.
FEATURES             Location/Qualifiers
     source          1..28
                     /organism="unidentified"
                     /db_xref="taxon:32644"
```

```
BASE COUNT        7 a      9 c      7 g      5 t
ORIGIN

  Query Match             100.0%;  Score 25;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db      27 AGGGACTTTCCGCTGGGGACTTTCC 3


RESULT 11
AR183747
LOCUS       AR183747                   29 bp    DNA     linear   PAT 28-APR-2002
DEFINITION  Sequence 4 from patent US 6348583.
ACCESSION   AR183747
VERSION     AR183747.1  GI:20287716
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ashkenazi,A.J.
  TITLE     Apo-2-receptor
  JOURNAL   Patent: US 6348583-A 4 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1..29
                     /organism="unknown"
BASE COUNT        4 a      8 c      9 g      8 t
ORIGIN

  Query Match             100.0%;  Score 25;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 12
AX099766
LOCUS       AX099766                   29 bp    DNA     linear   PAT 12-APR-2001
DEFINITION  Sequence 4 from Patent WO0119961.
ACCESSION   AX099766
VERSION     AX099766.1  GI:15144941
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ashkenazi,A.J., Chuntharapai,A. and Kim,K.J.
  TITLE     Apo-2 receptor antibodies
  JOURNAL   Patent: WO 0119961 A 4 22-MAR-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Sequence is synthesized"
BASE COUNT        4 a      8 c      9 g      8 t
ORIGIN

  Query Match             100.0%;  Score 25;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 13
AX188648
LOCUS       AX188648                   29 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from Patent WO0147533.
ACCESSION   AX188648
VERSION     AX188648.1  GI:15142254
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Hoeflich,K., Luo,J. and Woodgett,J.
  TITLE     Inhibition of gsk-3_g(b)
  JOURNAL   Patent: WO 0147533-A 1 05-JUL-2001;
            THE ONTARIO CANCER INSTITUTE (CA)
FEATURES             Location/Qualifiers
     source          1..29
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT        4 a      8 c      9 g      8 t
ORIGIN

  Query Match             100.0%;  Score 25;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       4 AGGGACTTTCCGCTGGGGACTTTCC 28


RESULT 14
AX188649/c
LOCUS       AX188649                   29 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from Patent WO0147533.
ACCESSION   AX188649
VERSION     AX188649.1  GI:15142255
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Hoeflich,K., Luo,J. and Woodgett,J.
  TITLE     Inhibition of gsk-3_g(b)
  JOURNAL   Patent: WO 0147533-A 1 05-JUL-2001;
            THE ONTARIO CANCER INSTITUTE (CA)
FEATURES             Location/Qualifiers
     source          1..29
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT        8 a      9 c      8 g      4 t
ORIGIN

  Query Match             100.0%;  Score 25;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db      26 AGGGACTTTCCGCTGGGGACTTTCC 2


RESULT 15
AR032342
LOCUS       AR032342                   29 bp    DNA     linear   PAT 27-JUL-1999
DEFINITION  Sequence 25 from patent US 5869955.
ACCESSION   AR032342
VERSION     AR032342.1  GI:5947947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

```
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Juan,S.-C., Lichenstein,H.S. and Wright,S.D.
  TITLE     Anti-inflammatory CD14 polypeptides
  JOURNAL   Patent: US 5869095-A 25 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="unknown"
BASE COUNT        5 a        9 c       11 g        8 t
ORIGIN
```

Query Match 100.0%; Score 25; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 AGGGACTTTCCGCTGGGGACTTTCC 25
           |||||||||||||||||||||||||
Db       6 AGGGACTTTCCGCTGGGGACTTTCC 30
```

Search completed: December 1, 2002, 08:21:32
Job time : 2710 secs